

86136

Access DB# 23

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

Requester's Full Name: Lisa V. CookExaminer #: 27134 Date: 2/5/03Art Unit: 1641 Phone Number 305-0808 Serial Number: 09/845,729Mail Box and Bldg/Room Location: CM1-7E12 Results Format Preferred (circle): PAPER DISK E-MAIL
9Pice CM1 7B-17

If more than one search is submitted, please prioritize searches in order of need:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Biopolymer marker indicative of disease state having a molecular weight of 1350 daltonsInventors (please provide full names): George Jackowski, Brad Thatcher, John Marshall, Tammy VreesEarliest Priority Filing Date: 4/30/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Sequence Search for: SE SDF LAE GGG VR

Seq. Id. No. 1

Sequence utility in detecting myocardial infarction or renal failure. Biopolymer marker/antibodies assay

also see attached claims + bib sheet

Thanks, ☺
L/Cook

RECEIVED
FEB -6 2003
STC

PL81 AAQ 13

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: Beverly c 4994NA Sequence (#) STN

Searcher Phone #:

AA Sequence (#) Dialog

Searcher Location:

Structure (#) Questel/Orbit

Date Searcher Picked Up:

Bibliographic Dr. Link Date Completed: 02-11-03Litigation Lexis/Nexis Searcher Prep & Review Time: 3Fulltext Sequence Systems

Serial Prep Time:

Patent Family WWW/Internet Online Time: 21Other Other (specify) CGN

THIS PAGE BLANK (USPTO)

Cook, L.
09/845729

09/845729

FILE "REGISTRY" ENTERED AT 09:18:47 ON 11 FEB 2003
L1 2 S SESDFLAEGGGV/SQSP

L1 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 474451-10-0 REGISTRY
CN Glycine, L-.alpha.-aspartyl-L-seryl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-aspartyl-L-phenylalanyl-L-leucyl-L-alanyl-L-.alpha.-glutamylglycylglycylglycyl-L-valyl-L-arginyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: US20020160420 PAGE: 12 unclaimed sequence
SQL 15

SEQ 1 DSESDFLAEG GGVRG
=====

HITS AT: 2-14

REFERENCE 1: 137:348834

L1 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 473552-35-1 REGISTRY
CN L-Arginine, L-seryl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-aspartyl-L-phenylalanyl-L-leucyl-L-alanyl-L-.alpha.-glutamylglycylglycylglycyl-L-valyl- (9CI) (CA INDEX NAME)
SQL 13

SEQ 1 SESDFLAEGG GVR
=====

HITS AT: 1-13

REFERENCE 1: 137:334901

FILE "HCAPLUS" ENTERED AT 09:19:16 ON 11 FEB 2003
L2 2 S L1

L2 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:833425 HCAPLUS
DOCUMENT NUMBER: 137:334901
TITLE: Alpha fibrinogen biopolymer marker indicative of myocardial infarction or renal failure having a molecular weight of 1350 daltons
INVENTOR(S): Jackowski, George; Thatcher, Brad; Marshall, John; Yantha, Jason; Vrees, Tammy
PATENT ASSIGNEE(S): Can.
SOURCE: U.S. Pat. Appl. Publ., 10 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160528	A1	20021031	US 2001-845729	20010430
WO 2002088722	A2	20021107	WO 2002-CA610	20020426
WO 2002088722	A3	20021227		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,			

Searcher : Shears 308-4994

THIS PAGE BLANK (USPTO)

09/845729

LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ,
BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

PRIORITY APPLN. INFO.:

US 2001-845729 A 20010430

AB The instant invention involves the use of a combination of preparatory steps in conjunction with mass spectroscopy and time-of-flight detection procedures to maximize the diversity of biopolymers which are verifiable within a particular sample. The cohort of biopolymers verified within such a sample is then viewed with ref. to their ability to evidence at least one particular disease state; thereby enabling a diagnostician to gain the ability to characterize either the presence or absence of said at least one disease state relative to recognition of the presence and/or the absence of said biopolymer. Serum samples were analyzed by SELDI-TOF using the Ciphergen PROTEINCHIP system and the disease specific marker identified by the sequence SESDFLAEGGGV and characterized as a .alpha. fibrinogen having a mol. wt. of 1350 daltons was found. This marker is indicative of myocardial infarction or renal failure.

IT 473552-35-1

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(alpha fibrinogen biopolymer marker of 1350 daltons indicative of myocardial infarction or renal failure)

L2 ANSWER 2 OF 2 HCPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:833395 HCPLUS

DOCUMENT NUMBER: 137:348834

TITLE: Process for diagnosis of physiological conditions by characterization of proteomic materials

INVENTOR(S): Jackowski, George; Thatcher, Brad; Marshall, John; Yantha, Jason; Vrees, Tammy

PATENT ASSIGNEE(S): Can.

SOURCE: U.S. Pat. Appl. Publ., 25 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160420	A1	20021031	US 2001-846330	20010430
WO 2002088744	A2	20021107	WO 2002-CA623	20020429
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				

THIS PAGE BLANK (USPTO)

09/845729

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-846330 A 20010430
AB The present invention discloses the use of proteomic investigation as a diagnostic tool; and particularly teaches the use of proteomic investigative techniques and methodol. to det. a proteomic basis for the development and progression of abnormal physiol. conditions and the development and characterization of risk assessment, diagnostic and therapeutic means and methodologies. Serum samples from patients suffering from a variety of diseases in Syndrome X were analyzed by SELDI mass spectrometry using the Ciphergen PROTEINCHIP system to discern disease markers.

IT **474451-10-0**

RL: PRP (Properties)
(unclaimed sequence; process for diagnosis of physiol. conditions by characterization of proteomic materials)

FILE 'HOME' ENTERED AT 09:19:25 ON 11 FEB 2003

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 16:00:57 ; Search time 354 Seconds

(without alignments)
23.677 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Pending Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PECTUS COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06 COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07 COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08 COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US081 COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US082 COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US083 COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US084 COMB.pep:*

9: /cgn2_6/ptodata/1/paa/US085 COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US086 COMB.pep:*

11: /cgn2_6/ptodata/1/paa/US087 COMB.pep:*

12: /cgn2_6/ptodata/1/paa/US088 COMB.pep:*

13: /cgn2_6/ptodata/1/paa/US089 COMB.pep:*

14: /cgn2_6/ptodata/1/paa/US090 COMB.pep:*

15: /cgn2_6/ptodata/1/paa/US091 COMB.pep:*

16: /cgn2_6/ptodata/1/paa/US092 COMB.pep:*

17: /cgn2_6/ptodata/1/paa/US093 COMB.pep:*

18: /cgn2_6/ptodata/1/paa/US094 COMB.pep:*

19: /cgn2_6/ptodata/1/paa/US095 COMB.pep:*

20: /cgn2_6/ptodata/1/paa/US096 COMB.pep:*

21: /cgn2_6/ptodata/1/paa/US097 COMB.pep:*

22: /cgn2_6/ptodata/1/paa/US098 COMB.pep:*

23: /cgn2_6/ptodata/1/paa/US099 COMB.pep:*

24: /cgn2_6/ptodata/1/paa/US100 COMB.pep:*

25: /cgn2_6/ptodata/1/paa/US101 COMB.pep:*

26: /cgn2_6/ptodata/1/paa/US102 COMB.pep:*

27: /cgn2_6/ptodata/1/paa/US60 COMB.pep:*

ALIGNMENTS

RESULT 1
US-09-845-725-1
; Sequence 1, Application US/09845725
; GENERAL INFORMATION:
; APPLICANT: JACKOWSKI, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1206 DALTONS
; FILE REFERENCE: 2132-028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

Query Match 87.7% ; Score 57; DB 22; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.0095;

Mismatches 1; Indels 0; Gaps 0;

Organism: Homo sapiens

US-09-845-725-1

Query Match 87.7% ; Score 57; DB 22; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0095;
Mismatches 1; Indels 0; Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	87.7	12	22 US-09-845-725-1	Sequence 1, App1
2	57	87.7	15	22 US-09-845-719A-1	Sequence 1, App1
3	57	87.7	16	8 PCT-US99-0350A-25	Sequence 25, App1
4	57	87.7	16	8 US-08-469-141-56	Sequence 56, App1
5	57	87.7	16	12 US-08-844-462-14	Sequence 14, App1
6	57	87.7	16	14 US-09-025-319A-25	Sequence 25, App1

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Qy 2 ESDPLAEGGGVR 13
Db 1 EGDLAEGGGVR 12

Sequence 1, Application US/09845719A
 GENERAL INFORMATION:
 APPLICANT: Jackowski, George
 TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR FILE REFERENCE: OF 1465 DALTONS
 CURRENT APPLICATION NUMBER: US/09/845,719A
 CURRENT FILING DATE: 2001-04-30
 NUMBER OF SEQ ID NOS: 1
 SEQ ID NO: 1
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-845-719A-1

Query Match 87.7%; Score 57; DB 22; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.012; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 1;

Qy 2 ESDFLAEGGGVR 13
 Db 4 EGDFLAEGGGVR 15

RESULT 3
 PCT-US99-03350A-25
 Sequence 25, Application PCT/US99/03350A
 GENERAL INFORMATION:
 APPLICANT: Yeaman, Michael R.
 APPLICANT: Shen, Alexander J.
 TITLE OF INVENTION: Antimicrobial Peptides And Derived Metapeptides
 NUMBER OF SEQUENCES: 95
 CORRESPONDENCE ADDRESS:
 ADDRESS: FULWIDER PATTON LEE & UTECHT, LLP
 STREET: 10877 Wilshire Blvd., Tenth Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90024

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 COMPUTER: Hewlett Packard
 OPERATING SYSTEM: WINDOWS 95
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US99/03350A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/025,319
 FILING DATE: February 18, 1998.
 ATTORNEY/AGENT INFORMATION:
 NAME: Drucker, I. Morley
 NAME: Parkhurst, David G.
 REGISTRATION NUMBER: 19,751
 REGISTRATION NUMBER: 29,422
 REFERENCE/DOCKET NUMBER: REI 50480
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (310) 824-5555
 TELEFAX: (310) 824-9696
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: no
 FRAGMENT TYPE: internal fragment
 FEATURE:
 NAME/KEY: CS-FBP"
 IDENTIFICATION METHOD: By experiment
 OTHER INFORMATION: microbcidal activities,

OTHER INFORMATION: PMIC = -78.53; MW = 1806.90; number of charged amino acids:
 PCT-US99-03350A-25
 Query Match 87.7%; Score 57; DB 1; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 4
 US-08-469-141-56
 Sequence 56, Application US/08469141
 GENERAL INFORMATION:
 APPLICANT: MUMFORD, RICHARD A.
 APPLICANT: DAVIES, D.T. PHILIP
 APPLICANT: DHALGREN, MARY E.
 APPLICANT: BOGER, JOSHUA S.
 APPLICANT: HOMES, JOHN L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DR. CHRISTINE B. CARTY
 STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,141
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CARTY, CHRISTINE B.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 174611B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)-594-6734
 TELEFAX: (908)-594-4720
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 FRAGMENT TYPE: internal
 US-08-469-141-56

Query Match 87.7%; Score 57; DB 8; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 5
 US-08-844-462-14
 Sequence 14, Application US/08844462
 GENERAL INFORMATION:
 APPLICANT: PATTERSON, DALE H.

APPLICANT: TARR, GEORGE E.
 TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patent Administrator - Testa, Hurwitz &
 STREET: High Street Tower, 125 High Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/844,462
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION NUMBER: 08/796,598
 FILING DATE: 07-FEB-1997
 APPLICATION NUMBER: US 08/446,055
 FILING DATE: 19-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: FLYNN EBG., Kerry A.
 REGISTRATION NUMBER: 33,683
 REFERENCE/DOCKET NUMBER: SYP-115
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-844-462-14

RESULT 6
 US-09-025-319A-25
 Sequence 25, Application US/09025319A
 GENERAL INFORMATION:
 APPLICANT: Yeaman, Michael R.
 APPLICANT: Shen, Alexander J.
 TITLE OF INVENTION: Antimicrobial Peptides And Derived Metapeptides
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 STREET: 10817 Wilshire Blvd., Tenth Floor
 CITY: Los Angeles
 STATE: California
 ZIP: 90024
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 COMPUTER: Hewlett Packard
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,319A

Query Match 87.7%; Score 57; DB 12; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 5 EGDFLAEKGGR 16

RESULT 6
 US-09-025-319A-25
 Sequence 25, Application US/09025319A
 GENERAL INFORMATION:
 APPLICANT: Yeaman, Michael R.
 APPLICANT: Shen, Alexander J.
 TITLE OF INVENTION: Antimicrobial Peptides And Derived Metapeptides
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 STREET: 10817 Wilshire Blvd., Tenth Floor
 CITY: Los Angeles
 STATE: California
 ZIP: 90024
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 COMPUTER: Hewlett Packard
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,319A

Query Match 87.7%; Score 57; DB 19; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 5 EGDFLAEKGGR 16

```

RESULT 8
; Sequence 25, Application US/09622561
; GENERAL INFORMATION: Yeaman, Michael R.
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; TITLE OF INVENTION: METAPEPTIDES
; FILE REFERENCE: 660081.415US
; CURRENT APPLICATION NUMBER: US/09/622,561
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
; OTHER INFORMATION: antimicrobicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-622-561-25

Query Match          Score 57;  DB 20;  Length 16;
Best Local Similarity 91.7%;  Pred. No. 0.013;
Matches 11;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy   2 ESDFLAEGGGVR 13
Db   5 EGDFLAEGGGVR 16

RESULT 9
; Sequence 25, Application US/09648816
; GENERAL INFORMATION: Yeaman, Michael R.
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED METAPEPTIDES
; FILE REFERENCE: 660081.415US
; CURRENT APPLICATION NUMBER: US/09/648,816
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/622,561
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US99/03350
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: fragment or analogue of PMP-1 or PMP-2
US-09-648-816-25

Query Match          Score 57;  DB 20;  Length 16;
Best Local Similarity 91.7%;  Pred. No. 0.013;
Matches 11;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy   2 ESDFLAEGGGVR 13
Db   5 EGDFLAEGGGVR 16

RESULT 10
; Sequence 25, Application US/09648816A
; GENERAL INFORMATION: Yeaman, Michael R.
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415US
; CURRENT APPLICATION NUMBER: US/09/648,816B
; NUMBER OF SEQ ID NOS: 111
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
; OTHER INFORMATION: antimicrobicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-648-816A-25

Query Match          Score 57;  DB 20;  Length 16;
Best Local Similarity 91.7%;  Pred. No. 0.013;
Matches 11;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy   2 ESDFLAEGGGVR 13
Db   5 EGDFLAEGGGVR 16

RESULT 11
; Sequence 109, Application US/09648816A
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415US
; CURRENT APPLICATION NUMBER: US/09/648,816A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/622,561
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 109
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
; OTHER INFORMATION: antimicrobicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-648-816A-109

Query Match          Score 57;  DB 20;  Length 16;
Best Local Similarity 91.7%;  Pred. No. 0.013;
Matches 11;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy   2 ESDFLAEGGGVR 13
Db   5 EGDFLAEGGGVR 16

RESULT 12
; Sequence 25, Application US/09648816B
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415US
; CURRENT APPLICATION NUMBER: US/09/648,816B
; NUMBER OF SEQ ID NOS: 111
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
; OTHER INFORMATION: antimicrobicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-648-816B-25

```

CURRENT FILING DATE: 2000-08-25
 PRIORITY APPLICATION NUMBER: US 09/622,561
 PRIOR FILING DATE: 2000-08-18
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 25
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
 OTHER INFORMATION: microbial domains from platelet microbial
 OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits.
 US-09-648-816B-25

Query Match Score 57; DB 20; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013; 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 5 EGDFLAEGGGR 16

RESULT 13
 US-09-657-276-1135
 Sequence 1135, Application US/09657276
 GENERAL INFORMATION:
 1 APPLICANT: Coniuchem, Inc.
 1 APPLICANT: Bridon, Dominique
 1 APPLICANT: Ezrin, Alan
 1 APPLICANT: Milner, Peter
 1 APPLICANT: Holmes, Darren
 2 APPLICANT: Thibaudeau, Karen
 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
 TITLE OF INVENTION: COMPONENTS
 FILE REFERENCE: 2110
 CURRENT APPLICATION NUMBER: US/09/657,276
 CURRENT FILING DATE: 2000-09-07
 PRIOR APPLICATION NUMBER: 60/134,406
 PRIOR FILING DATE: 1999-05-17
 PRIOR APPLICATION NUMBER: 60/153,406
 PRIOR FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: 60/159,783
 PRIOR FILING DATE: 1999-10-18
 NUMBER OF SEQ ID NOS: 1617
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1135
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide

US-09-657-276-1135
 Query Match Score 57; DB 20; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013; 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 5 EGDFLAEGGGR 16

RESULT 14
 US-09-826-290-352
 Sequence 352, Application US/09826290
 GENERAL INFORMATION:
 1 APPLICANT: Durham, L. Kathryn
 1 APPLICANT: Friedman, David L.
 1 APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

US-09-845-765-1
 Query Match Score 57; DB 22; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.013; 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 5 EGDFLAEGGGR 16

Search completed: February 10, 2003, 16:13:47
 Job time : 356 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query	Match	Length	DB	ID	Description
1	65	100.0	13	5	US-09-845-729-1		Sequence 1, Appli
2	57	87.7	16	6	US-10-325-162-1		Sequence 1, Appli
3	57	87.7	70	5	US-09-724-576-71849		Sequence 71849, A
4	57	87.7	70	5	US-09-724-576-71849		Sequence 71849, A
5	57	87.7	93	5	US-09-724-676-71847		Sequence 71847, A
6	57	87.7	388	6	US-10-236-392-34		Sequence 34, Appli
7	57	87.7	481	6	US-10-293-510-45		Sequence 5, Appli
8	57	87.7	644	6	US-10-310-154-381		Sequence 32, Appli
9	57	87.7	644	6	US-10-236-392-32		Sequence 6, Appli
10	57	87.7	866	1	PCT-US02-37760-6		Sequence 302, App
11	57	87.7	866	1	PCT-US02-37760-6		Sequence 455, App
12	57	87.7	866	5	US-09-949-002-302		Sequence 45, App
13	57	87.7	875	5	US-09-949-002-455		Sequence 45, App
14	46	70.8	17	6	US-10-310-154-381		Sequence 381, App
15	40	61.5	489	6	US-09-950-084-5126		Sequence 5126, App
16	39	60.0	286	5	US-09-950-084-5126		Sequence 5898, App
17	38	58.5	115	5	US-09-513-99C-5198		Sequence 62455, A
18	38	58.5	320	5	US-09-724-576-62455		Sequence 62455, A
19	38	58.5	320	5	US-09-724-676-62455		Sequence 62456, A
20	38	58.5	325	5	US-09-724-576A-52456		Sequence 62456, A
21	38	58.5	608	1	PCT-US02-35563-27		Sequence 27, Appli
22	38	58.5	611	6	US-10-223-089-340		Sequence 340, App
23	38	58.5	671	5	US-09-724-576-62453		Sequence 62453, A
24	38	58.5	671	5	US-09-724-676A-52453		Sequence 62453, A
25	38	58.5	676	5	US-09-724-676-62454		Sequence 62454, A
26	38	58.5	676	5	US-09-724-676A-62454		Sequence 62452, A
			27	38	58.5	722	5 US-09-724-676-62452
			28	38	58.5	722	5 US-09-724-676-62452
			29	38	58.5	722	5 US-09-724-676-62452
			30	37	56.9	381	6 US-10-099-056-1416
			31	36	55.4	11	6 US-10-212-499-39
			32	36	55.4	175	6 US-10-264-337-1928
			33	36	55.4	311	5 US-09-724-676-75821
			34	36	55.4	311	5 US-09-724-676A-57821
			35	36	55.4	426	6 US-10-203-138A-13561
			36	36	55.4	500	6 US-10-288-798-4
			37	36	55.4	611	7 US-60-428-082-19
			38	36	55.4	1268	6 US-10-76-774-2166
			39	36	55.4	1472	5 US-09-724-676-7022
			40	36	55.4	1472	5 US-09-724-676A-57022
			41	36	55.4	1493	5 US-09-724-676-57021
			42	36	55.4	1493	5 US-09-724-676A-57021
			43	36	55.4	1583	1 PCT-US02-32727-15149
			44	36	55.4	1583	6 US-10-057-498-15149
			45	36	55.4	1783	6 US-10-275-140-4

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 3
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 71849
 LENGTH: 70
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-724-676-71849

Query Match 87.7%; Score 57; DB 5; Length 70;
 Best Local Similarity 91.7%; Pred. No. 0.034;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 24 EGDFLAEGGGVR 35

RESULT 4
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676A
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 71849
 LENGTH: 70
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-724-676-71849

Query Match 87.7%; Score 57; DB 5; Length 70;
 Best Local Similarity 91.7%; Pred. No. 0.034;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 24 EGDFLAEGGGVR 35

RESULT 5
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 71849
 LENGTH: 93
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-724-676-71847
 Sequence 71847, Application US/09724676A

RESULT 6
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676A
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 71847

Query Match 87.7%; Score 57; DB 5; Length 93;
 Best Local Similarity 91.7%; Pred. No. 0.045;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 42 EGDFLAEGGGVR 53

RESULT 7
 US-10-236-392-34
 Sequence 71847, Application US/10236392
 GENERAL INFORMATION:
 APPLICANT: Anderson, David W
 APPLICANT: Boldog, Ferenc L
 APPLICANT: Burgess, Catherine, E
 APPLICANT: Casman, Stacie J
 APPLICANT: Catterton, Elina
 APPLICANT: Chapiro, Andrei
 APPLICANT: Crabtree, Julie
 APPLICANT: Edinger, Shlomit, R
 APPLICANT: Ellerman, Karen
 APPLICANT: Gerlach, Valerie
 APPLICANT: Gorman, Linda
 APPLICANT: Gross, William M
 APPLICANT: Gusev, Vladamir
 APPLICANT: Kekuda, Ramesh
 APPLICANT: Larchelle, William J
 APPLICANT: Li, Li
 APPLICANT: Macdougall, John R
 APPLICANT: Malynkar, Uriel M
 APPLICANT: Miller, Charles E
 APPLICANT: Millet, Isabelle
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Paturajan, Meera
 APPLICANT: Pena, Carol A
 APPLICANT: Peyman, John A
 APPLICANT: Raselli, Luca
 APPLICANT: Reiger, Daniel K
 APPLICANT: Rothenberg, Mark E
 APPLICANT: Sheroy, Suresh
 APPLICANT: Shinkets, Richard A
 APPLICANT: Smitson, Glenda
 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-442A

CURRENT APPLICATION NUMBER: US/10/236,392
 CURRENT FILING DATE: 2002-09-06
 PRIOR APPLICATION NUMBER: US/9/540,763
 PRIOR FILING DATE: 2000-03-30
 PRIOR APPLICATION NUMBER: US/6/390,155
 PRIOR FILING DATE: 2002-06-19
 PRIOR APPLICATION NUMBER: US/9/635,949
 PRIOR FILING DATE: 2000-08-10
 PRIOR APPLICATION NUMBER: US/6/318,765
 PRIOR FILING DATE: 2001-09-12
 PRIOR APPLICATION NUMBER: US/6/357,303
 PRIOR FILING DATE: 2002-02-15
 PRIOR APPLICATION NUMBER: US/6/367,753
 PRIOR FILING DATE: 2002-03-25
 PRIOR APPLICATION NUMBER: US/6/369,479
 PRIOR FILING DATE: 2002-04-02
 PRIOR APPLICATION NUMBER: US/9/659,634
 PRIOR FILING DATE: 2000-09-12
 PRIOR APPLICATION NUMBER: US/6/318,120
 PRIOR FILING DATE: 2001-09-07
 PRIOR APPLICATION NUMBER: US/6/318,130
 PRIOR FILING DATE: 2001-09-07
 REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PALM.
 NUMBER OF SEQ ID NOS: 794
 SOFTWARE: Custom
 SEQ ID NO: 34
 LENGTH: 388
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-236-392-34

Query Match 87.7%; Score 57; DB 6; Length 388;
 Best Local Similarity 91.7%; Pred. No. 0.18;
 Matches 11; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 24 EGDFLAEGGVR 35

RESULT 8
 US-10-236-392-36
 GENERAL INFORMATION:
 APPLICANT: Anderson, David W
 APPLICANT: Boldog, Ferenc L
 APPLICANT: Burgess, Catherine E
 APPLICANT: Casman, Stacie J
 APPLICANT: Catterton, Elina
 APPLICANT: Chapatval, Andrei
 APPLICANT: Crabtree, Julie
 APPLICANT: Edinger, Shlomit, R
 APPLICANT: Ellerman, Karen
 APPLICANT: Gerlach, Valerie
 APPLICANT: Gorman, Linda
 APPLICANT: Grossie, William M
 APPLICANT: Gusev, Vladimir
 APPLICANT: Kekuda, Ramesh
 APPLICANT: LaRochelle, William J
 APPLICANT: Li, Li
 APPLICANT: Macdougal, John R
 APPLICANT: Malyankar, Uriel M
 APPLICANT: Miller, Charles E
 APPLICANT: Millet, Isabelle
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Patturajan, Meera
 APPLICANT: Pena, Carol A
 APPLICANT: Peyman, John A
 APPLICANT: Rastelli, Luca
 APPLICANT: Reiger, Daniel K
 APPLICANT: Rothenberg, Mark E
 APPLICANT: Shenoy, Suresh
 APPLICANT: Shimkets, Richard A

APPLICANT: Smithson, Glenda
 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 2140-442A
 CURRENT APPLICATION NUMBER: US/10/236,392
 CURRENT FILING DATE: 2002-09-06
 PRIOR APPLICATION NUMBER: US/9/540,763
 PRIOR FILING DATE: 2000-03-30
 PRIOR APPLICATION NUMBER: US/6/390,155
 PRIOR FILING DATE: 2002-06-19
 PRIOR APPLICATION NUMBER: US/9/635,949
 PRIOR FILING DATE: 2000-08-10
 PRIOR APPLICATION NUMBER: US/6/357,303
 PRIOR FILING DATE: 2002-02-15
 PRIOR APPLICATION NUMBER: US/6/367,753
 PRIOR FILING DATE: 2002-03-25
 PRIOR APPLICATION NUMBER: US/6/369,479
 PRIOR FILING DATE: 2002-04-02
 PRIOR APPLICATION NUMBER: US/9/659,634
 PRIOR FILING DATE: 2000-09-12
 PRIOR APPLICATION NUMBER: US/6/318,120
 PRIOR FILING DATE: 2001-09-07
 PRIOR APPLICATION NUMBER: US/6/318,130
 REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PALM.
 NUMBER OF SEQ ID NOS: 794
 SOFTWARE: Custom
 SEQ ID NO: 36
 LENGTH: 481
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-236-392-36

Qy 2 ESDFLAEGGVR 13
 Db 24 EGDFLAEGGVR 35

RESULT 9
 PCT-US02-37760-5
 Sequence 5, Application PCT-US0237760
 GENERAL INFORMATION:
 APPLICANT: GENVEC, INC.
 APPLICANT: KESSLER, PAUL D
 APPLICANT: KOVSEDI, IMRE
 TITLE OF INVENTION: ANGIOPOIETIN RELATED FACTORS
 FILE REFERENCE: 220091
 CURRENT APPLICATION NUMBER: PCT/US02/37760
 CURRENT FILING DATE: 2002-11-21
 PRIOR APPLICATION NUMBER: US 60/334488
 PRIOR FILING DATE: 2001-11-30
 NUMBER OF SEQ ID NOS: 174
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 5
 LENGTH: 644
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US02-37760-5

Query Match 87.7%; Score 57; DB 1; Length 644;
 Best Local Similarity 91.7%; Pred. No. 0.28;
 Matches 11; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 24 EGDFLAEGGVR 35

RESULT 10
US-10-236-392-32
GENERAL INFORMATION:
Sequence 32, Application US/10236392
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Catterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Crabtree, Julie
APPLICANT: Edinger, Shlomit, R
APPLICANT: Ellerman, Karen
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Gross, William M
APPLICANT: Gusev, Vladamir
APPLICANT: Kekuda, Ramesh
APPLICANT: LaRochelle, William J
APPLICANT: Li, Li
APPLICANT: MacDougall, John R
APPLICANT: Malyanikar, Uriel M
APPLICANT: Miller, Charles E
APPLICANT: Miller, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Pattaajan, Meera
APPLICANT: Pena, Carol A
APPLICANT: Peyman, John A
APPLICANT: Rastelli, Luca
APPLICANT: Reiger, Daniel K
APPLICANT: Rothenberg, Mark E
APPLICANT: Shenoy, Suresh
APPLICANT: Shmikets, Richard A
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: THERAPEUTIC POLYPPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 214-02-442A
CURRENT APPLICATION NUMBER: US/10/236, 392
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US/0/340,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US/0/390,155
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/0/635,949
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US/0/318,765
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/0/357,303
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US/0/367,753
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US/0/369,479
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US/9/659,634
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US/0/318,120
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
SEQ ID NO: 32
LENGTH: 644
TYPE: PRT
ORGANISM: Homo sapiens
US-10-236-392-32

Query Match 87.7%; Score 57; DB 6; Length 644;
Best Local Similarity 91.7%; Pred. No. 0.28;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDPLAEGGVR 13

RESULT 11
PCT-US02-37760-6
Sequence 6, Application PC/TUS0237760
GENERAL INFORMATION:
APPLICANT: KOVSEDI, IMRE
APPLICANT: GENYVC, INC.
APPLICANT: KESSLER, PAUL D
APPLICANT: KOVSEDI, IMRE
TITLE OF INVENTION: ANGIOPOIETIN RELATED FACTORS
FILE REFERENCE: 220091
CURRENT APPLICATION NUMBER: PCT/US02/37760
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/334488
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 866
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-37760-6

Query Match 87.7%; Score 57; DB 1; Length 866;
Best Local Similarity 91.7%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDPLAEGGVR 13

Db 24 EGDFLAEKGVR 35

RESULT 12
US-09-949-002-302
Sequence 302, Application US/09949002
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10523
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 302
LENGTH: 866
TYPE: PRT
ORGANISM: Human
US-09-949-002-302

Query Match 87.7%; Score 57; DB 5; Length 866;
Best Local Similarity 91.7%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDPLAEGGVR 13

Db 24 EGDFLAEKGVR 35

RESULT 13
US-09-949-002-455
Sequence 455, Application US/09949002
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28
 PRIORITY APPLICATION NUMBER: 60/231,401
 PRIORITY FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 10823
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 455
 LENGTH: 875
 TYPE: PRT
 ORGANISM: Human
 US-09-949-002-455

RESULT 14

Query Match 87.7%; Score 57; DB 5; Length 875;
 Best Local Similarity 91.7%; Pred. No. 0.38;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 33 EGDFLAEGGGVR 44

US-10-293-580-45

Sequence 45, Application US/10293580

GENERAL INFORMATION:
 APPLICANT: Aurora Biosciences Corporation

APPLICANT: Cubitt, Andrew B.

TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications

FILE REFERENCE: AURO1270 (08366.031001)

CURRENT APPLICATION NUMBER: US/10/283,580

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: US/09/129,192

PRIOR FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.0

SEQ ID NO: 45
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: thrombin

US-10-293-580-45

Query Match 70.8%; Score 46; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FLAEGGGVR 13
 Db 1 FLAEGGGVR 9

Jung, Vincent
 Kretzmer, Keith A.
 Lacette, Lucille B.
 Lai, Chao-Qiang
 Lee, Gary
 Lin, Jie-Yi
 Liu, Jingdong
 Lu, Bin
 Luehby, Michael M.
 Lund, Adrian
 Madison, Linda L.
 Mailoy, Kathleen A.
 McKiel, Christine L.
 Miller, Philip W.
 Padmavathi, Manchikanti
 Partiell, Laurence D.
 Start, William G.
 Temnesen, Dan
 Vidyka, K. R.
 Wang, Haiyun
 Xin, Zhanqiao
 Xu, Nanfei
 Yang, Chunzhi
 Zeng, Xiaopang
 Zhang, Qiang
 Zhao, Yajuan
 Zhou, Li

TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants

FILE REFERENCE: 38-15 (52796) B

CURRENT APPLICATION NUMBER: US/10/310,154

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/337,358

PRIOR FILING DATE: 2001-12-04

NUMBER OF SEQ ID NOS: 736

SEQ ID NO: 381
 LENGTH: 489
 TYPE: PRT
 ORGANISM: Zea mays

US-10-310-154-381

Query Match 61.5%; Score 40; DB 6; Length 489;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SESDFLAGGGVR 13
 Db 419 TSKDFMAGGGLR 431

Search completed: February 10, 2003, 16:14:54

Job time : 61 secs

RESULT 15

US-10-310-154-381

Sequence 381, Application US/10310154

GENERAL INFORMATION:
 APPLICANT: Edgerton, Michael D
 APPLICANT: Chomet, Paul S.
 APPLICANT: Adams, Thomas H
 APPLICANT: Ruff, Thomas G.
 APPLICANT: Agarwal, Ameeta K.
 APPLICANT: Ahrens, Jeffrey E.
 APPLICANT: Ball, James A.
 APPLICANT: Banu, G.
 APPLICANT: Bell, Erin
 APPLICANT: Boddupalli, Raghava
 APPLICANT: Deikman, Jill
 APPLICANT: Deng, Mojian
 APPLICANT: Dong, Jinzhuo
 APPLICANT: Galligan, Meghan M.
 APPLICANT: Hincher, Brenda S.
 APPLICANT: Huang, Shihshieh
 APPLICANT: Johnson, G. Richard

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3									
Copyright (c) 1993 - 2003 Compugen Ltd.									
I protein - protein search, using SW model									
run on: February 10, 2003, 15:55:46 ; Search time 82 Seconds (without alignments) 21.125 Million cell updates/sec									
title: US-09-845-729-1									
Perfect score: 65	Sequence: 1 SESDFLAEGGVR 13	Scoring table: BLOSUM62	Gapop 10.0 , Gapext 0.5	Searched: 908470 seqs, 133250620 residues	Total number of hits satisfying chosen parameters: 908470	Post-processing: Minimum Match 0%	Maximum Match 0%	Listing First 45 summaries	
Maximum DB seq length: 0 Minimum DB seq length: 2000000000									
Database : A_Geneseq_101002:*									
1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*	2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*	3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*	4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*	5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*	6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*	7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*	8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*	9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*	10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*	12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*	13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*	14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*	15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*	16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*	17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*	18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*	19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*	20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*	22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*	23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.9	Human API-118 tryp	PR	XX	XX	XX
5	57	87.7	16	22 ABB5233.7	Fibrinogen fragme	PA	XX	XX	XX
6	57	87.7	16	22 ABB91959	Fibrinogen epitope	PI	XX	XX	XX
7	57	87.7	17	17 AAR96184	Fibrinectin fragme	PI	XX	XX	XX
8	57	87.7	17	22 ABB91950	Fibrinogen epitope	PI	XX	XX	XX
9	57	87.7	18	17 AAR96193	Fibrinogen epitope	PI	XX	XX	XX
10	57	87.7	19	17 AAR96192	Fibrinogen epitope	PI	XX	XX	XX
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	OS	XX	XX	XX
1	57	87.7	16	17 AAR96194	Fibrinogen epitope	OS	XX	XX	XX
2	57	87.7	16	18 AAW04619	Fibrinopeptide A p	PN	XX	XX	XX
3	57	87.7	16	20 AYB7487	Vascular dementia	PP	XX	XX	XX
4	57	87.7	16	22 ABB5622.					

Query Match 87.7%; Score 57; DB 20; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 4

ABB5219
 ID ABB5219 standard; Peptide; 16 AA.

XX

AC ABB5219;

XX

DT 15-FEB-2002 (first entry)

XX

DE Vascular dementia-associated protein isoform (VPI) 419.

XX

KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;

XX

KW diagnosis; prognosis; gene therapy.

XX

OS Homo sapiens.

XX

PN WO2001169261-A2.

XX

PD 20-SEP-2001.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PP 14-MAR-2001; 2001WO-GB01106.

XX

PR 15-MAR-2000; 2000GB-0006285.

XX

PR 24-NOV-2000; 2000GB-0028734.

XX

PR 28-NOV-2000; 2000US-0724391.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Herath HMAC, Parekh RB, Rohlf C;

XX

DR WPI; 2001-557937/62.

XX

PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprising analysing body fluid by 2-dimensional electrophoresis for features correlated with VD.

XX

PT Claim 6; Page 39; 151pp; English.

XX

CC The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABB5219-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy.

XX

SQ Sequence 16 AA;

XX

Query Match 87.7%; Score 57; DB 22; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SQ Sequence 16 AA;

XX

Query Match 87.7%; Score 57; DB 22; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

Query Match 87.7%; Score 57; DB 22; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

Query Match 87.7%; Score 57; DB 22; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

Query Match 87.7%; Score 57; DB 22; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

Query Match 87.7%; Score 57; DB 22; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

RESULT 5
 ABB52337
 ID ABB52337 standard; Peptide; 16 AA.

Qy 2 ESDFLAEGGGVR 13

Db 5 EGDFLAEGGGVR 16

RESULT 6

AAB91959
 ID AAB91959 standard; Peptide; 16 AA.

XX

AC AAB91959;

XX

DT 08-FEB-2002 (first entry)

XX

DE Human API-118 tryptic digest peptide #2.

XX

KW Human; neuroprotective; nootropic; gene therapy; vaccine;

XX

KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; API;

XX

KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;

XX

KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX

OS Homo sapiens.

XX

PN WO200175154-A2.

XX

PD 11-OCT-2001.

XX

PP 03-APR-2001; 2001WO-US10908.

XX

PR 03-APR-2000; 2000US-194504P.

XX

PR 28-NOV-2000; 2000US-25347P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PA (PFIZER INC.

XX

PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;

XX

PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX

PI Townsend RR, White F, Williams SA;

XX

WPI; 2001-639384/73.

XX

PT Screening for Alzheimer's disease in a mammal, by making

XX

PT two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of

XX

PT healthy persons -

XX

PS Example; Page 33; 162pp; English.

XX

CC The invention relates to methods for the screening, diagnosis and

XX

CC prognosis of Alzheimer's disease. The methods involve the detection

XX

CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's

XX

CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,

XX

CC serum or plasma. The abundance of the AFs and APIs is then

XX

CC normalised to an Expression Reference Protein Isoform (ERPI) in

XX

CC order to determine whether a patient is suffering from, or has

XX

CC a predisposition to, Alzheimer's Disease. The relative abundance of

XX

CC the AFs and APIs correlates with the severity of Alzheimer's Disease.

XX

CC The present sequence is a peptide produced from an API by proteolysis.

XX

CC Sequence 16 AA;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87.7%; Score 57; DB 22; Length 16;

XX

CC Best Local Similarity 91.7%; Pred. No. 0.004; Indels 1; Gaps 0;

XX

CC Query Match 87

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; neurotransmitter.
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PP 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudreau K;
 XX
 DR WPI: 2001-112055/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptide degradation, useful for increasing length of in vivo activity
 PT
 PT Disclosure; Page 567; 733pp; English.
 PS
 PS Page 567; 733pp; English.

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxy/thiol groups on blood components to form a peptide stabilised therapeutic peptide composed of 3-50 amino acids (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB9029 to AAB9241 represent peptides which can be used in the exemplification of the present invention.

XX Sequence 16 AA;

Query Match 87.7%; Score 57; DB 22; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 ID AAR96184 standard; peptide; 17 AA.
 Db 5 EGDFLAEGGGVR 16

RESULT 7
 AAR96184
 ID AAR96184 standard; peptide; 17 AA.
 XX
 AC AAR96184;
 DT 19-DEC-1996 (first entry)

DB Fibrinogen epitope probe, represents alpha chain residues 5-21.
 XX Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen; monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid; sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis; pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;

XX chronic obstructive pulmonary disease; myelogenous leukaemia;
 KW infantile respiratory distress syndrome; gout;
 KW adult respiratory distress syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9614580-A1.
 XX
 PD 17-MAY-1996.
 XX
 PP 03-NOV-1995; 95WO-US13794.
 XX
 PR 06-JUN-1995; 95US-0469141.
 PR 07-NOV-1994; 94US-0335524.
 XX
 PA (MERK) MERCK & CO INC.
 XX
 PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
 XX
 DR WPI: 1996-251088/25.
 XX
 PT New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX
 PS Example 5; Page 41; 109pp; English.
 XX
 CC The sequences given in AAR96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other fibrinogen cleavage
 CC products. The monospecific antibodies may be used to assay for the
 CC formation of complementary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
 XX
 SQ Sequence 17 AA;
 SQ
 Query Match 87.7%; Score 57; DB 17; Length 17;
 Best Local Similarity 91.7%; Pred. No. 0.0043; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 ID AAB91960 standard; peptide; 17 AA.
 ID AAB91960
 XX
 AC AAB91960;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1136.
 DE
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069300-A2.
 XX
 PD 23-NOV-2000.

DR WPI: 1996-251888/25.
 XX New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX
 PS Example 5; Page 42; 109pp; English.
 XX The sequences given in AAR96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other fibrinogen cleavage
 CC products. The monospecific antibody may be used to assay for the
 CC formation of complementary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome, and myelogenous leukaemia. See also AAR96146-81.
 XX
 SQ Sequence 19 AA;
 Query Match 87.7%; Score 57; DB 17; Length 19;
 Best Local Similarity 91.7%; Pred. No. 0.0048; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 12
 ID AAR96191
 ID AAR96191 standard; peptide; 20 AA.
 XX
 AC AAR96191;
 XX
 DT 19-DEC-1996 (first entry)
 XX Fibrinogen epitope probe, represents alpha chain residues 1-20.
 DE
 XX Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
 KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
 KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
 KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
 KW chronic obstructive pulmonary disease; myelogenous leukaemia;
 KW infantile respiratory distress syndrome; gout;
 KW adult respiratory distress syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO9614580-A1.
 XX
 PD 17-MAY-1996.
 XX
 PA 03-NOV-1995; 95WO-US13794.
 XX
 PR 06-JUN-1995; 95US-0469141.
 PR 07-NOV-1994; 94US-0335524.
 PA (MERI) MERCK & CO INC.
 XX
 PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA.
 XX
 PR 1996-251888/25.
 DR
 PT New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX
 PS Example 5; Page 42; 109pp; English.

XX The sequences given in AAR96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other fibrinogen cleavage
 CC products. The monospecific antibody may be used to assay for the
 CC formation of complementary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
 XX
 SQ Sequence 20 AA;
 Query Match 87.7%; Score 57; DB 17; Length 20;
 Best Local Similarity 91.7%; Pred. No. 0.0051; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 13
 ID AAY57488
 ID AAY57488 standard; Peptide; 20 AA.
 XX
 AC AAY57488;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide CS-FBP-alpha-TET SEQ ID NO:26.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PR 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1998; 98US-0025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI: 1999-522717/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 CC against bacteria and fungi -
 XX
 Disclosure; Page 120; 16pp; English.
 XX
 PS
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXKB and its derivatives
 CC selected from XBZBAXBXKB, XBZKZXB and XBZBZBX; and
 CC (b) a second peptide template XBZXX and their derivatives selected from
 CC the group consisting of XBZBXB, XBZKXB, XBZBZBX, XBZXXB, and
 CC XBZBAXZBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and

fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention.

XX Sequence 20 AA;

Query Match 87.7%; Score 57; DB 20; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.0051; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEKGGRV 16

RESULT 14
AAFP90276

ID AAF90276 standard; peptide; 22 AA.

XX AC AAF90276;

XX DT 17-MAY-1990 (first entry)

XX DB 19-DEC-1996 (first entry)

XX DB Fibrinogen epitope probe, represents alpha chain residues 1-21.

XX KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;

XX KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;

XX KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;

XX KW pulmonary oedema; chronic bronchitis; cystic fibrosis; bronchiectasis;

XX KW chronic obstructive pulmonary disease; myelogenous leukaemia;

XX KW infantile respiratory distress syndrome; gout;

XX KW adult respiratory distress syndrome.

OS Homo sapiens.

XX PN WO9614580-A1.

XX PD 17-MAY-1996.

XX PF 03-NOV-1995; 95WO-US13794.

XX PR 06-JUN-1995; 95US-046141.

XX PR 07-NOV-1994; 94US-0335524.

XX PA (MERI) MERCK & CO INC.

XX PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;

XX DR WPI; 1996-251888/25.

XX PT New isolated fibrinogen derived cleavage products - used for detection of leukocyte elastase activity in disease diagnosis and for evaluating elastase inhibitors

XX PS Example 5; Page 41; 109pp; English.

XX The sequences given in AAR96182-94 represent antigenic probes derived

CC from the first 21 amino acids of human fibrinogen. These probes are

CC used to determine antibody titre against other fibrinogen cleavage

CC products. The monospecific antibodies may be used to assay for the

CC formation of complementarity cleavage product antigens or epitopes in

CC whole blood or other body fluids, peritoneal fluid, sputum or

CC bronchoalveolar lavage fluid. The assay for cleavage products is

CC dependent upon the presence of HLE in the sample. This assay can also

CC be used for the evaluation of HLE inhibitors. The antibodies may be

CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary

CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive

CC pulmonary disease, bronchiectasis, adult or infantile respiratory

CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.

XX Sequence 21 AA;

CC Query Match 87.7%; Score 57; DB 10; Length 22;

CC Best Local Similarity 91.7%; Pred. No. 0.0056;

CC Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC Qy 2 ESDFLAEGGGVR 13

CC Db 5 EGDFLAEKGGRV 16

CC RESULT 15

CC AAR96182

CC ID AAR96182 standard; peptide; 22 AA.

CC XX AC AAR96182;

CC SQ Sequence 22 AA;

CC Query Match 87.7%; Score 57; DB 10; Length 22;

CC Best Local Similarity 91.7%; Pred. No. 0.0056;

CC Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC Qy 2 ESDFLAEGGGVR 13

CC Db 5 EGDFLAEKGGRV 16

DT 19-DEC-1996 (first entry)
 DE Fibrinogen epitope probe, represents alpha chain residues -1-21.
 XX Epitope; cleavage product; leukocyte elastase; HLE; fibrinogen;
 KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
 KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
 KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
 KW chronic obstructive pulmonary disease; myelogenous leukaemia;
 KW infantile respiratory distress syndrome; gout;
 KW adult respiratory distress syndrome.
 XX OS Homo sapiens.
 PN WO9614580-A1.
 XX PD 17-MAY-1996.
 XX PP 03-NOV-1995; 95WO-US13794.
 XX PR 06-JUN-1995; 95US-0469141.
 PR 07-NOV-1994; 94US-0335524.
 XX PA (MERCK & CO INC.
 XX PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
 XX DR 1996-251988/25.
 XX PT New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX PS Example 5; Page 41; 109pp; English.

XX The sequences given in AAR96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other Fibrinogen Cleavage
 CC products. The monospecific antibodies may be used to assay for the
 CC formation of complimentary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
 XX SQ Sequence 22 AA;

Query Match 87.7%; Score 57; DB 17; Length 22;
 Best Local Similarity 91.7%; Pred. No. 0.0056; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1;

Qy 2 ESDFLAEGGGYR 13
 Db 6 EGDFLAEGGGYR 17

Search completed: February 10, 2003, 16:00:48
 Job time : 83 secs

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 15:59:27 ; Search time 15 Seconds (without alignments)

25.500 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SBSDFLAEGG3YR 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

28 57 87.7 643 2 US-08-551-356-4
29 57 87.7 643 5 PCT-US93-12687-4
30 57 87.7 644 1 US-08-206-176-2
31 57 87.7 847 4 US-09-373-157-4
32 52 80.0 15 5 PCT-US95-13794-6
33 52 80.0 15 5 PCT-US95-13794-6
34 52 80.0 28 6 5196404-16
35 47 72.3 10 6 5196404-18
36 47 72.3 10 6 5433940-25
37 46 70.8 17 2 US-08-792-553-11
38 46 70.8 24 2 US-08-978-404B-8
39 40 61.5 13 3 US-08-1469-141A-4/7
40 40 61.5 13 5 PCT-US95-13794-7
41 36 55.4 11 3 US-08-592-500-19
42 36 55.4 11 3 US-08-195-006-39
43 36 55.4 11 5 PCT-US94-07644A-39
44 36 55.4 14 4 US-08-860-808E-1
45 36 55.4 420 1 US-08-391-259-7

RESULT 1
US-08-796-598-14
; Sequence 14, Application US/08796598
; Patent No. 5827639
; GENERAL INFORMATION:
; APPLICANT: PETERSON, DALE H.
; APPLICANT: TARR, GEORGE E.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; NUMBER OF SEQUENCES: 23
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,598
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,055
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FLYNN ESG, KERTY A.
; REGISTRATION NUMBER: 33,693
; REFERENCE/DOCKET NUMBER: SYP-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-796-598-14

Query Match 87.7% ; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length DB	ID	Description
1	57	87.7	16	2 US-08-796-598-14	Sequence 14, App1
2	57	87.7	16	2 US-08-447-175A-14	Sequence 14, App1
3	57	87.7	16	3 US-08-141A-56	Sequence 56, App1
4	57	87.7	16	5 PCT-US95-13794-56	Sequence 56, App1
5	57	87.7	17	3 US-08-469-141A-46	Sequence 46, App1
6	57	87.7	17	5 PCT-US95-13794-46	Sequence 46, App1
7	57	87.7	18	3 US-08-469-141A-55	Sequence 55, App1
8	57	87.7	18	5 PCT-US95-13794-55	Sequence 55, App1
9	57	87.7	19	3 US-08-141A-54	Sequence 54, App1
10	57	87.7	Sequence 54, App1		
11	57	87.7	20	1 US-08-288-657-1	Sequence 1, App1
12	57	87.7	20	1 US-07-984-884-1	Sequence 1, App1
13	57	87.7	20	1 US-08-481-810-1	Sequence 1, App1
14	57	87.7	20	1 US-08-484-426-1	Sequence 1, App1
15	57	87.7	20	2 US-08-480-818-1	Sequence 1, App1
16	57	87.7	20	3 US-08-469-141A-53	Sequence 53, App1
17	57	87.7	20	5 PCT-US95-13794-53	Sequence 53, App1
18	57	87.7	21	3 US-08-469-141A-45	Sequence 45, App1
19	57	87.7	21	5 PCT-US95-13794-45	Sequence 45, App1
20	57	87.7	22	3 US-08-469-141A-44	Sequence 44, App1
21	57	87.7	22	3 US-08-469-141A-52	Sequence 52, App1
22	57	87.7	22	5 PCT-US95-13794-44	Sequence 44, App1
23	57	87.7	22	5 PCT-US95-13794-52	Sequence 52, App1
24	57	87.7	23	4 US-08-160-808E-25	Sequence 25, App1
25	57	87.7	25	4 US-08-440-522-16	Sequence 16, App1
26	57	87.7	25	4 US-08-440-331-16	Sequence 9, App1
27	87.7	30	2 US-07-963-538B-9		

Qy 2 ESDFLAEGGGYR 13
 Db 5 EGDFLAEGGGYR 16

RESULT 2

US-08-447-175A-14

; Sequence 14, Application US/08447175A

; Patent No. 5863240

GENERAL INFORMATION:

; APPLICANT: PATTERSON, DALE H.

; ADDRESS: Patent Administrator - Testa, Hurwitz &

; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING

; POLYMERS WITH A STATISTICAL CERTAINTY USING MASS

; SPECTROMETRY.

; NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

; NAME: Rauschenbach, Kurt

; REGISTRATION NUMBER: 40,137

; REFERENCE/DOCKET NUMBER: SYP-114

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; CURRENT APPLICATION NUMBER: US/08/447,175A

; FILING DATE: 19-NOV-1995

; CLASSIFICATION: 422

ATTORNEY/AGENT INFORMATION:

; NAME: RAUSCHENBACH, Kurt

; REGISTRATION NUMBER: 40,137

; REFERENCE/DOCKET NUMBER: SYP-114

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; CURRENT APPLICATION NUMBER: US/08/447,175A

; FILING DATE: 19-NOV-1995

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; US-08-447-175A-14

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLEC

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-6734
 TELEFAX: (908) 594-4720
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 PCT-US95-13794-56

Query Match 87.7%; Score 57; DB 5; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00089;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 5
 US-08-469-141A-46
 Sequence 46, Application US/08469141A
 Patent No. 6,124,107

GENERAL INFORMATION:
 APPLICANT: MUMFORD, RICHARD A.
 APPLICANT: DAVIES, D. T. PHILIP
 APPLICANT: DAHLGREN, MARY E.
 APPLICANT: BOGER, JOSHUA S.
 APPLICANT: HOMES, JOHN L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESS: DR. CHRISTINE E. CARTY
 STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0907

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US95/13794
 FILING DATE: 03-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Carty, Christine E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 17461IAY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-6734
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 PCT-US95-13794-46

Query Match 87.7%; Score 57; DB 5; Length 17;
 Best Local Similarity 91.7%; Pred. No. 0.00095;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
 PCT-US95-13794-46
 Sequence 46, Application PCT-US9513794
 GENERAL INFORMATION:
 APPLICANT: Mumford, Richard A.
 APPLICANT: Davies, D. T. Phillip
 APPLICANT: Dahlgren, Mary E.
 APPLICANT: Boger, Joshua S.
 APPLICANT: Humes, John L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESS: Dr. Christine E. Carty
 STREET: 126 E. Lincoln Avenue; P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0907

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US95/13794
 FILING DATE: 03-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Carty, Christine E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 17461IAY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-6734
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 PCT-US95-13794-46

Query Match 87.7%; Score 57; DB 5; Length 17;
 Best Local Similarity 91.7%; Pred. No. 0.00095;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 US-08-469-141A-55
 Sequence 55, Application US/08469141A
 Patent No. 6,124,077
 GENERAL INFORMATION:
 APPLICANT: Mumford, Richard A.
 APPLICANT: Davies, D. T. Phillip
 APPLICANT: Dahlgren, Mary E.
 APPLICANT: Boger, Joshua S.

Query Match 87.7%; Score 57; DB 3; Length 17;

US-08-469-141A-46

APPLICANT: HUMES, JOHN L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 NUMBER OF SEQUENCES: 71
 ADDRESSEE: DR. CHRISTINE E. CARTY
 STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07065-0507
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER:
 APPLICATION NUMBER: US/08/469,141A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CARTY, CHRISTINE E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 17461IAY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)-594-6734
 TELEFAX: (908)-594-4720
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal

RESULT 8
 PCT-US95-13794-55
 Sequence 55, Application PC/TUS9513794
 GENERAL INFORMATION:
 APPLICANT: Mumford, Richard A.
 APPLICANT: Davies, D.T. Philip
 APPLICANT: Dahlgren, Mary E.
 APPLICANT: Boger, Joshua S.
 APPLICANT: Humes, John L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dr. Christine E. Carty
 STREET: 126 E. Lincoln Avenue; P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0507
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,141A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CARTY, CHRISTINE E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 17461IAY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)-594-6734
 TELEFAX: (908)-594-4720
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-469-141A-54

Query Match Score 87.7%; Pred. No. 0.0011; Length 19;
 Best Local Similarity 91.7%; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEAGGGVR 16

RESULT 10
 PCT-US95-13794-54
 Sequence 54, Application PC/TUS9513794
 GENERAL INFORMATION:
 APPLICANT: Mumford, Richard A.
 APPLICANT: Davies, D.T. Philip
 APPLICANT: Dahlgren, Mary E.
 APPLICANT: Boser, Joshua S.
 APPLICANT: Humes, John L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dr. Christine E. Carty
 STREET: 1226 E. Lincoln Avenue; P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0907

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13794
 FILING DATE: 03-NOV-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Carty, Christine E.
 REGISTRATION NUMBER: 36,039
 REFERENCE/DOCKET NUMBER: 174611AY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-4720
 TELEFAX: (908) 594-6734
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 PCT-US95-13794-54

Query Match Score 87.7%; Pred. No. 0.0011; Length 19;
 Best Local Similarity 91.7%; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEAGGGVR 16

RESULT 11
 US-08-288-657-1

Query Match Score 87.7%; Pred. No. 0.0011; Length 19;
 Best Local Similarity 91.7%; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 1; Mismatches 1; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEAGGGVR 16

RESULT 12
 US-07-384-884-1
 Sequence 1, Application US/07984884
 GENERAL INFORMATION:
 APPLICANT: Teger-Nilsson, Ann-Catrine E
 APPLICANT: Bylund, Ruth E

TITLE OF INVENTION: New peptide derivatives
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: White and Case
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036-2787

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/984,884
 FILING DATE: 02-DEC-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sterner, Richard J
 REGISTRATION NUMBER: 35, 372
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 354-8200
 TELEFAX: (212) 354-8113

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal

US-07-984-884-1

Query Match Score 57%; DB 1; Length 20;
 Best Local Similarity 91.7%; Pred. No. 0.0011; Indels 0;
 Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 EGDFLAEGGGVR 16

RESULT 13
 US-08-481-810-1

Sequence 1, Application US/08481810
 Patent No. 5736521
 GENERAL INFORMATION:
 APPLICANT: Teger-Nilsson, Ann-Catrine E
 CORRESPONDENCE ADDRESS:
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036-2787

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,426

FILING DATE: Classification: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/984884
 FILING DATE: 02-DEC-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sterner, Richard J
 REGISTRATION NUMBER: 35, 372
 REFERENCE/DOCKET NUMBER: US 07/984884
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ANTI-SENSE: NO

US-08-481-426-1

Query Match Score 57%; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 0.0011; Mismatches 0; Indels 1; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 15
US-08-480-818-1

Sequence 1, Application US/08480818
Patent No. 555433

GENERAL INFORMATION:
APPLICANT: Teger-Nilsson, Ann-Catrine E
APPLICANT: Bylund, Ruth E

TITLE OF INVENTION: New peptide derivatives
NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: United States
ZIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,818
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984884

FILING DATE: 02-DEC-1992
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Stern, Richard J

REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-016

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200

TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

US-08-480-818-1

Query Match Score 57; DB 2; Length 20;

Best Local Similarity 91.7%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

Search completed: February 10, 2003, 16:07:45
Job time : 16 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw mode1

Run on: February 10, 2003, 16:02:52 ; Search time 29 Seconds
 (without alignments)
 11.453 Million cell updates/sec

Title: US-09-845-729-1
 Perfect score: 65
 Sequence: 1 SRSDFLAEQQGYR 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/prodata/1/pubpaas/US08_NEW_PUB.pep:
 2: /cgn2_6/prodata/1/pubpaas/PCT_NEW_PUB.pep:
 3: /cgn2_6/prodata/1/pubpaas/US06_NEW_PUB.pep:
 4: /cgn2_6/prodata/1/pubpaas/US07_NEW_PUB.pep:
 5: /cgn2_6/prodata/1/pubpaas/US05_PUBCOMB.pep:
 6: /cgn2_6/prodata/1/pubpaas/US07_PUBCOMB.pep:
 7: /cgn2_6/prodata/1/pubpaas/US08_PUBCOMB.pep:
 8: /cgn2_6/prodata/1/pubpaas/US08_PUBCOMB.pep:
 9: /cgn2_6/prodata/1/pubpaas/US09_NEW_PUB.pep:
 10: /cgn2_6/prodata/1/pubpaas/US10_PUBCOMB.pep:
 11: /cgn2_6/prodata/1/pubpaas/US10_NEW_PUB.pep:
 12: /cgn2_6/prodata/1/pubpaas/US10_PUBCOMB.pep:
 13: /cgn2_6/prodata/1/pubpaas/US60_NEW_PUB.pep:
 14: /cgn2_6/prodata/1/pubpaas/US60_PUBCOMB.pep:
 15: /cgn2_6/prodata/1/pubpaas/US63_AP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	87.7	12	9 US-09-845-725-1	Sequence 1, Appli
2	57	87.7	15	9 US-09-845-719A-1	Sequence 1, Appli
3	57	87.7	16	9 US-09-846-780-1	Sequence 1, Appli
4	57	87.7	16	9 US-09-726-230-352	Sequence 16, Appli
5	57	87.7	25	9 US-09-757-774-16	Sequence 58?, Appli
6	57	87.7	360	10 US-09-925-297-587	Sequence 4, Appli
7	57	87.7	847	9 US-10-112-521-4	Sequence 1, Appli
8	52	80.0	10	9 US-09-846-350-1	Sequence 1, Appli
9	52	80.0	11	9 US-09-846-342-1	Sequence 1, Appli
10	46	70.8	17	9 US-10-057-505-11	Sequence 11, Appli
11	42	64.6	98	10 US-09-740-668A-18	Sequence 18, Appli
12	39	60.0	1164	10 US-09-834-792-5	Sequence 5, Appli
13	39	60.0	1165	9 US-10-126-188-8	Sequence 8, Appli
14	39	60.0	2039	9 US-10-192-504-7	Sequence 7, Appli
15	38	58.5	154	10 US-09-925-300-1763	Sequence 1763, Appli
16	36	55.4	359	9 US-09-772-758-2	Sequence 2, Appli
17	36	55.4	359	10 US-09-745-663-34	Sequence 34, Appli
18	36	55.4	426	10 US-09-864-761-42921	Sequence 4221, Appli
19	35.5	54.6	418	9 US-09-738-626-5679	Sequence 5679, Appli

ALIGNMENTS

RESULT 1
 US-09-845-725-1
 Sequence 1, Application US-09845725
 ; Patent No. US20020161185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jackowski, George
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
 ; TITLE OF INVENTION: OF 1206 DALTONS
 ; FILE REFERENCE: 2132-028
 ; CURRENT APPLICATION NUMBER: US-09-845-725
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 12;
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-845-725-1

Query Match 87.7%; Score 57; DB 9; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0012; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
 US-09-845-719A-1
 Sequence 1, Application US-09845719A
 ; Patent No. US20020161179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jackowski, George
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
 ; TITLE OF INVENTION: OF 1465 DALTONS
 ; FILE REFERENCE: 2132-035
 ; CURRENT APPLICATION NUMBER: US-09-845-719A
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1

LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-845-719A-1

Query Match 87.7%; Score 57; DB 9; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.0015; Indels 0;
 Matches 11; Conservative 0; Mismatches 1; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 4 EGDFLAEGGGR 15

RESULT 3
 US-09-846-780-1
 ; Sequence 1, Application US/09846780
 ; Patent No. US2002010423A1
 ; GENERAL INFORMATION
 ; APPLICANT: Jackowski, George
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
 ; FILE REFERENCE: 2132.039
 ; CURRENT APPLICATION NUMBER: US/09/846.780
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-846-780-1

Query Match 87.7%; Score 57; DB 9; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.0016; Indels 0;
 Matches 11; Conservative 0; Mismatches 1; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 5 EGDFLAEGGGR 16

RESULT 4
 US-09-826-290-352
 ; Sequence 352, Application US/09826290
 ; Patent No. US20020164668A1
 ; GENERAL INFORMATION
 ; APPLICANT: Durham, L.Kathryn
 ; APPLICANT: Friedman, David L.
 ; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
 ; APPLICANT: Kimmel, Lida H.
 ; APPLICANT: Parekh, Rakesh Bhikhu
 ; APPLICANT: Potter, David M.
 ; APPLICANT: Rohlf, Christian
 ; APPLICANT: Silber, B. Michael
 ; APPLICANT: Stiger, Thomas R.
 ; APPLICANT: Sunderland, P. Trey
 ; APPLICANT: Townsend, Robert Reid
 ; APPLICANT: White, Frost
 ; APPLICANT: Williams, Stephen A.
 ; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
 ; TITLE OF INVENTION: Alzheimer's Disease
 ; FILE REFERENCE: 25722-1-001 N2
 ; CURRENT APPLICATION NUMBER: US/09/826.290
 ; PRIOR APPLICATION NUMBER: US 60/194,504
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: US 60/253,547
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 492
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 352

Query Match 87.7%; Score 57; DB 9; Length 25;
 Best Local Similarity 91.7%; Pred. No. 0.0025; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 7 EGDFLAEGGGR 18

RESULT 5
 US-09-757-774-16
 ; Sequence 16, Application US/09757774
 ; Publication No. US20020181756A1
 ; GENERAL INFORMATION
 ; APPLICANT: Dintzis, Howard M.
 ; APPLICANT: Blodgett, James S.
 ; APPLICANT: Cheronis, John
 ; TITLE OF INVENTION: THERAPEUTIC SUPPRESSION OF SPECIFIC IMMUNE RESPONSES BY
 ; TITLE OF INVENTION: ADMINISTRATION OF OLIGOMERIC FORMS OF ANTIGEN OF CONTROLLED
 ; TITLE OF INVENTION: CHEMISTRY
 ; FILE REFERENCE: 07265/124004
 ; CURRENT APPLICATION NUMBER: US/09/757,774
 ; CURRENT FILING DATE: 2000-01-09
 ; PRIOR APPLICATION NUMBER: US 08/440,322
 ; PRIOR FILING DATE: 1995-05-12
 ; PRIOR APPLICATION NUMBER: US 07/808,797
 ; PRIOR FILING DATE: 1991-12-17
 ; PRIOR APPLICATION NUMBER: US 07/628,858
 ; PRIOR FILING DATE: 1990-12-17
 ; PRIOR APPLICATION NUMBER: US 08/354,710
 ; PRIOR FILING DATE: 1989-05-22
 ; PRIOR APPLICATION NUMBER: US 07/248,293
 ; PRIOR FILING DATE: 1988-09-21
 ; PRIOR APPLICATION NUMBER: US 06/869,808
 ; PRIOR FILING DATE: 1986-05-29
 ; PRIOR APPLICATION NUMBER: US 06/460,266
 ; PRIOR FILING DATE: 1983-01-24
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1) ..(25)
 ; OTHER INFORMATION: Xaa = O-ACA/Pro

Query Match 87.7%; Score 57; DB 9; Length 25;
 Best Local Similarity 91.7%; Pred. No. 0.0025; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGR 13
 Db 7 EGDFLAEGGGR 18

RESULT 6
 US-09-926-297-587
 ; Sequence 587, Application US/09925297
 ; Patent No. US20020081659A1
 ; GENERAL INFORMATION
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA105
 ; CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10
 PRIORITY APPLICATION NUMBER: PCT/US00/05989
 PRIOR FILING DATE: 2000-03-08
 PRIORITY APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 928
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 587
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: NAME/KEY: SITE
 LOCATION: (15)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (315)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (325)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (326)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (327)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (339)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-297-587

Query Match Score 87.7%; DB 10; Length 360;
 Best Local Similarity 91.7%; Pred. No. 0.036; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1;

Qy 2 ESDFLAEGGVR 13
 Db 45 EGDFLAEGGVR 56

RESULT 7
 US-10-112-527-4
 Sequence 4, Application US/10112527
 Patent No. US20020168722A1
 GENERAL INFORMATION:
 APPLICANT: Grieninger, Gerd
 APPLICANT: Applegate, Dianne
 APPLICANT: Stoike-Stoben, Lara
 TITLE OF INVENTION: No. US20020168722A1el Cleaved Fragments of Fibrinogen
 FILE REFERENCE: Docket 454 24 CON
 CURRENT FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 09/373,157
 PRIOR FILING DATE: 1999-08-12
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 4
 LENGTH: 847
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-112-527-4

Query Match Score 87.7%; DB 9; Length 847;
 Best Local Similarity 91.7%; Pred. No. 0.086; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1;

Qy 2 ESDFLAEGGVR 13
 Db 5 EGDFLAEGGVR 16

RESULT 8

US-09-846-350-1
 Sequence 1, Application US/09846350
 Patent No. US2002016188A1
 GENERAL INFORMATION:
 APPLICANT: Jackowski, George
 TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having a Molecular
 TITLE OF INVENTION: of 1020 Daltons
 FILE REFERENCE: 2132 025
 CURRENT APPLICATION NUMBER: US/09/846,350
 CURRENT FILING DATE: 2001-04-30
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-846-350-1

Query Match Score 80.0%; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0063;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DELAEGGVR 13
 Db 1 DELAEGGVR 10

RESULT 9
 US-09-846-342-1
 Sequence 1, Application US/09846342
 Patent No. US20020160422A1
 GENERAL INFORMATION:
 APPLICANT: Jackowski, George
 TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
 TITLE OF INVENTION: OF 1077 DALTONS
 FILE REFERENCE: 2132-026
 CURRENT APPLICATION NUMBER: US/09/846,342
 CURRENT FILING DATE: 2001-04-30
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-846-342-1

Query Match Score 80.0%; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DELAEGGVR 13
 Db 2 DELAEGGVR 11

RESULT 10
 US-10-057-505-11
 Sequence 11, Application US/10057505
 Patent No. US20020164674A1
 GENERAL INFORMATION:
 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 APPLICANT: AURORA BIOSCIENCES CORPORATION
 APPLICANT: Tsien, Roger
 APPLICANT: Heim, Roger
 APPLICANT: Cubitt, Andrew
 TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
 FILE REFERENCE: REGN1260-3
 CURRENT APPLICATION NUMBER: US/10/057,505
 CURRENT FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: US 08/792,553
 PRIOR FILING DATE: 1997-01-31
 PRIOR APPLICATION NUMBER: US 09/396,003
 PRIOR FILING DATE: 1999-09-13

NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 11
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Linker moiety
 US-10-057-505-11

Query Match 70.8%; Score 46; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 5 FLAEGGGVR 13
 Db 1 FLAEGGGVR 9

RESULT 11
 US-09-740-668A-18
 Sequence 18, Application US/09740668A.
 / Patent No. US20020076700A1
 / GENERAL INFORMATION:
 / APPLICANT: Shimkets, Richard
 / TITLE OF INVENTION: No. US20020076700A1 polypeptides and nucleic acids encoding same
 / FILE REFERENCE: 15966-537 CIP
 / CURRENT APPLICATION NUMBER: US/09/740,668A
 / CURRENT FILING DATE: 2000-12-18
 / PRIOR APPLICATION NUMBER: PCT/US99/29584
 / PRIOR FILING DATE: 1999-12-17
 / PRIOR APPLICATION NUMBER: 09/465,512
 / PRIOR FILING DATE: 1999-12-16
 / PRIOR APPLICATION NUMBER: 60/113,485
 / PRIOR FILING DATE: 1999-12-21
 / PRIOR APPLICATION NUMBER: 60/112,837
 / PRIOR FILING DATE: 1998-12-18
 / NUMBER OF SEQ ID NOS: 98
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 18
 / LENGTH: 98
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-740-668A-18

Query Match 64.6%; Score 42; DB 10; Length 98;
 Best Local Similarity 63.6%; Pred. No. 2.7;
 Matches 7; Conservative 3; Mismatches 1; Indels 0;
 Gaps 0;

Qy 3 SDFLAEQQV 13
 Db 50 ADFLGQQGGVQ 60

RESULT 12
 US-09-834-792-5
 / Sequence 5, Application US/09834792
 / Patent No. US20020037515A1
 / GENERAL INFORMATION:
 / APPLICANT: Mount Sinai School of Medicine of NYU
 / TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
 / FILE REFERENCE: AP32911 070165.0589
 / CURRENT APPLICATION NUMBER: US/09/834,792
 / CURRENT FILING DATE: 2001-04-13
 / PRIOR APPLICATION NUMBER: 60/197,491
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / LENGTH: 1164
 / TYPE: PRT
 / ORGANISM: Human

US-09-834-792-5
 Query Match 60.0%; Score 39; DB 10; Length 1164;
 Best Local Similarity 61.5%; Pred. No. 1e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;

Qy 1 SESDFLAEQQV 13
 Db 1117 SVAVDLAQGGPR 1129

RESULT 13
 US-10-026-188-8
 / Sequence 8, Application US/10026188
 / Patent No. US20050164645A1
 / GENERAL INFORMATION:
 / APPLICANT: Zhang, Yifeng
 / APPLICANT: The Regents of the University of California
 / TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
 / TITLE OF INVENTION: Assays for Ion Channel
 / FILE REFERENCE: 02307E-1149101S
 / CURRENT APPLICATION NUMBER: US/10/026,188
 / CURRENT FILING DATE: 2001-12-21
 / PRIOR APPLICATION NUMBER: US 60/259,379
 / PRIOR FILING DATE: 2000-12-29
 / NUMBER OF SEQ ID NOS: 8
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO 8
 / LENGTH: 1165
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: human ltrpc6
 US-10-026-188-8

Query Match 60.0%; Score 39; DB 9; Length 1165;
 Best Local Similarity 61.5%; Pred. No. 1e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;

Qy 1 SESDFLAEQQV 13
 Db 1118 SVAVDLAQGGPR 1130

RESULT 14
 US-10-192-584-7
 / Sequence 7, Application US/10192584
 / Publication No. US20030027987A1
 / GENERAL INFORMATION:
 / APPLICANT: TOKUNAGA, Eiji
 / APPLICANT: MATSUO, Kazuo
 / APPLICANT: HANADA, Fukusaburo
 / APPLICANT: TOKIYOSHI, Sachio
 / TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
 / NUMBER OF SEQUENCES: 8
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: BROWND AND NEIMARK
 / STREET: 624 Ninth Street, N.W., Suite 300
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: USA
 / ZIP: 20001
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/10/192,584
 / FILING DATE: 11-Jul-2002

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/077,098
 FILING DATE: 19-MAY-1998
 APPLICATION NUMBER: PCT/JP97/02222
 FILING DATE: 12-SEP-1997
 APPLICATION NUMBER: JP 27,148/1996
 FILING DATE: 19-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: KORNBAU, Anne M.
 REGISTRATION NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-678-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2039 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-192-584-7

Query Match 60.0%; Score 39; DB 9; Length 2039;
 Best Local Similarity 61.5%; Pred. No. 1.8e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 SESDFLAEGGGR 13
 Db 786 SEIDLQNGGCV 798

RESULT 15
 US-09-925-300-1763
 Sequence 1763, Application US/09925300
 Patent No. US20020151681A1
 GENERAL INFORMATION:
 APPLICANT: Craig Rosen,
 ATTORNEY: Steve Ruben
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA101
 CURRENT APPLICATION NUMBER: US/09/925,300
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05988
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 1763
 LENGTH: 154
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (147)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 US-09-925-300-1763
 Query Match 58.5%; Score 38; DB 10; Length 154;
 Best Local Similarity 72.7%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SESDFLAEGGG 11
 Db 28 SLTDFLAEDGG 38

THIS PAGE BLANK (USPTO)

Copyright (c) 1993 - 2003	GenCore version 5.1.3	Compugen Ltd.	30	38	58.5	669	2	A72718
OM protein - protein search, using sw model			31	38	58.5	686	2	T08919
Run on:	February 10, 2003, 15:58:46 ; Search time 16 Seconds (without alignments) 78.109 Million cell updates/sec		32	38	58.5	727	2	T08920
Title:	US-09-845-729-1		33	38	58.5	742	2	T00371
Perfect score:	65		34	37	56.9	149	2	G85534
Sequence:	1 SESDFLAEGGGVR 13		35	37	56.9	149	2	C90684
Scoring table:	BLOSUM62		36	37	56.9	164	2	E70639
Gapopen:	10.0	Gapext 0.5	37	37	56.9	302	2	F90526
Searched:	283224 seqs, 96134422 residues		38	37	56.9	363	2	G71544
Total number of hits satisfying chosen parameters:	283224		39	37	56.9	410	2	F96683
Minimum DB seq length: 0			40	37	56.9	412	2	S28423
Maximum DB seq length: 2000000000			41	37	56.9	415	2	S65065
Post-processing: Minimum Match 0%			42	37	56.9	416	2	S47013
Maximum Match 100%			43	37	56.9	416	2	A96585
Database :	PIR 73;* 1: pir1;* 2: pir2;* 3: pir3;* 4: pir4;*		44	37	56.9	421	2	D69643
Post-processing: Minimum Match 0%			45	37	56.9	433	2	T09619
Listing first 45 summaries								ALIGNMENTS
Result No.	Score	Query Match	Length	DB	ID	Description		
1	61	93.8	16	2	H29501	fibrinopeptide A -		RESULT 1
2	57	87.7	16	2	C28854	fibrinopeptide A -		H29501
3	57	87.7	16	2	A24180	fibrinogen alpha C		
4	57	87.7	16	2	B24180	fibrinogen alpha C		
5	57	87.7	16	2	A28854	fibrinopeptide A -		
6	57	87.7	16	2	B28854	fibrinopeptide A -		
7	57	87.7	16	2	A29501	fibrinopeptide A -		
8	57	87.7	16	1	F0HUA	fibrinogen alpha C		
9	57	87.7	866	2	D44234	fibrinogen alpha C		
10	52	80.0	15	2	P29501	fibrinopeptide A -		
11	51	78.5	16	2	G29501	fibrinopeptide A -		
12	51	78.5	28	2	A05296	fibrinogen alpha C		
13	49	75.4	17	2	B29501	fibrinopeptide A -		
14	48	73.8	15	2	B29501	fibrinopeptide A -		
15	48	73.8	19	2	C29501	fibrinopeptide A -		
16	48	73.8	19	2	C29501	fibrinopeptide A -		
17	48	73.8	311	2	A05294	fibrinogen alpha C		
18	40	61.5	15	2	JP0101	fibrinogen alpha C		
19	40	61.5	280	2	H9800	hypothetical prote		
20	39	60.0	236	2	S48867	dimeethylallyltrans		
21	39	60.0	245	2	AG0701	Orf 245 protein [i		
22	39	60.0	271	2	S18730	amino-glycoside N3'		
23	39	60.0	324	2	D70943	hypothetical prote		
24	39	60.0	705	2	T31157	probable secreted		
25	38.5	59.2	732	2	AB2732	probable homeodomain		
26	38.5	59.2	741	2	B97513	translation initia		
27	38	58.5	575	2	T48224	hypothetical prote		
28	38	58.5	611	1	S12566	probable secreted		
29	38	58.5	652	2	AD2316	probable homeodomain		
						N; Contains: fibrinopeptide A		
						Fragment)		

C;Species: *Macaca fuscata* (Japanese macaque)
 C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 26-Jan-1996
 C;Accession: A2180
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J.; Biochem. 97, 1487-1492, 1985
 A;Title: Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and patas monkey (E
 uenos, and baboons.
 A;Reference number: A91990; MUID:85289140; PMID:3928610
 A;Accession: A24180
 A;Molecule type: protein
 A;Residues: 1-16 <NAK>
 C;Superfamily: Fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGVR 13
 Db 5 ECDFLAEGGGVR 16

RESULT 4

B24180
 fibrinogen alpha chain - red guenon (fragment)
 N;Contains: fibrinopeptide A
 C;Species: *Brythrocercus patas* (red guenon, hussar)
 C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
 C;Accession: B24180
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J.; Biochem. 97, 1487-1492, 1985
 A;Title: Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and patas monkey (E
 uenos, and baboons.
 A;Reference number: A91990; MUID:85289140; PMID:3928610
 A;Accession: B24180
 A;Molecule type: protein
 A;Residues: 1-16 <NAK>
 C;Superfamily: Fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGVR 13
 Db 5 ECDFLAEGGGVR 16

RESULT 5

A28854
 Fibrinopeptide A - olive baboon
 C;Species: *Papio anubis*, *Papio hamadryas anubis* (olive baboon)
 C;Date: 19-May-1988 #sequence_revision 19-May-1988 #text_change 26-Jan-1996
 C;Accession: A28854
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J.; Biochem. 94, 1973-1978, 1983
 A;Title: Fibrinopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*, and *Theropit
 A;Reference number: A91973; MUID:84161822; PMID:6423621
 A;Accession: A28854
 A;Molecule type: protein
 A;Residues: 1-16 <NAK>
 C;Superfamily: Fibrinogen alpha chain; fibrinogen disulfide ring homology*

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGVR 13
 Db 5 ECDFLAEGGGVR 16

RESULT 6

R;Rixon, M.W.; Chan, W.Y.; Davie, B.W.; Chung, D.W.

B28854
 Fibrinopeptide A - hamadryas baboon
 C;Species: *Papio hamadryas* (hamadryas baboon)
 C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
 C;Accession: B28854
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J.; Biochem. 94, 1973-1978, 1983
 A;Title: Fibrinopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*, and *Theropit
 A;Reference number: A91973; MUID:84161822; PMID:6423621
 A;Accession: B28854
 A;Molecule type: protein
 A;Residues: 1-16 <NAK>
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology*

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ESDFLAEGGGVR 13
 Db 5 ECDFLAEGGGVR 16

RESULT 7

A29501
 Fibrinopeptide A - baboon
 C;Species: *Papio* sp. (baboon)
 C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
 C;Accession: A29501
 R;Blombaeck, B.; Blombaeck, M.; Hann, C.
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
 A;Reference number: A29501
 A;Accession: A29501
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <BL0>
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 Db 5 ECDFLAEGGGVR 16

RESULT 8

FGHUA
 fibrinogen alpha chain precursor, short splice form [validated] - human
 N;Alternate names: coagulation factor I
 N;Contains: fibrinopeptide A
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
 C;Accession: A93956; A41568; A90468; I84456; A44234; C44234; B94433; A90433; B94309; S19
 C;Accession: A93956; A41568; A90468; I84456; A44234; C44234; B94433; A90433; B94309; S19
 R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3955-3957, 1983
 A;Title: Partial mRNA sequences for human Alpha₁Bbeta₁ and gamma fibrinogen chains: ev
 A;Reference number: A93956; MUID:83247396; PMID:6575389
 A;Accession: A93956
 A;Molecule type: mRNA
 A;Residues: 1-64 <KAN>
 A;Cross-references: GB:J00128; NID:9182425; PID:AA52427.1; PID:9182426
 R;Chung, D.W.; Harris, J.E.; Davie, E.W.
 Adv. Exp. Med. Biol. 281, 39-48, 1990
 A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
 A;Reference number: A43568; MUID:91344740; PMID:2102623
 A;Accession: A43568
 A;Molecule type: DNA
 A;Residues: 1-330; 'A', 332-644 <CHU>
 A;Cross-references: GB:964988; NID:9458553; PID:AA17055.1; PMID:9458554
 R;Rixon, M.W.; Chan, W.Y.; Davie, B.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983
 A;Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha A;Reference number: A90466; MUID:828342; PMID:6388355

A;Molecule type: mRNA
 A;Residues: 1-330, 'A', 332-629 <RIK>
 A;Cross-references: GB:J00127; PIDN:AAA52426.1; PMID:9182423
 R; Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
 Nucleic Acids Res. 11, 7427-7434, 1983
 A;Title: Isolation and characterization of cDNA clones for the Aalpha- and gamma-chains A;Reference number: I37333; MUID:84069777; PMID:6689067

A;Molecule type: mRNA
 A;Residues: 110-156 <RES>
 A;Cross-references: GB:KG2272; NID:9182427; PIDN:AAA52428.1; PMID:9182428
 R; Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redman, Biochemistry 31, 11968-11972, 1992
 A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel A;Reference number: A44234; MUID:93090725; PMID:1457396
 A;Accession: A44234
 A;Molecule type: mRNA
 A;Residues: 1-51 <F01>
 A;Cross-references: GB:MG4982; NID:9458553; PIDN:AAA17055.1; PMID:9458554
 A;Accession: C44234
 A;Status: not compared with conceptual translation
 A;Cross-references: GB:MG4982; NID:9458553; PIDN:AAA17055.1; PMID:9458554
 A;Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIP:119914, NCBIP:119918)
 R; Henschel, A.; Lottspeich, F.; Soutan, C.; Topfer-Petersen, E.
 in: Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp. 51-56, Pe A;Reference number: A94433
 A;Accession: B94433
 A;Molecule type: protein
 A;Residues: 20-214, 'RS', 217-298, 'G', 300-303, 'G', 305-629 <HEN>
 R; Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
 Biochemistry 18, 5410-5416, 1979
 A;Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlapping A;Reference number: A94433; MUID:80088231; PMID:518846
 A;Contents: disulfide bonds
 A;Accession: A90433
 A;Molecule type: protein
 A;Residues: 20-146, 'Q', 148-198, 'N', 197-230, 'N', 232-316, 'SG', 319-406, 'D', 408, 'N', 410-629
 R; Blomback, B.; Hessel, B.; Hogg, D.
 Thromb. Res. 8, 639-658, 1976
 A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A;Reference number: A94309; MUID:76225080; PMID:336108
 A;Accession: S19297
 A;Contents: variant, and disulfide bonds
 A;Molecule type: protein
 A;Residues: 20-40 <DEW>
 R; Rezzios, A.D.; Markland Jr., F.S.
 Thromb. Res. 52, 541-552, 1988
 A;Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co A;Reference number: A60905; MUID:89162316; PMID:3232124
 A;Molecule type: protein
 A;Residues: 433-451 <RET>
 R; Freito, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
 J. Biol. Chem. 253, 2184-2195, 1978
 A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
 A;Reference number: A92225; MUID:78130085; PMID:632262

A;Contents: annotation; cross-linking acceptor sites
 R; Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
 Biochemistry 18, 5405-5410, 1979
 A;Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat A;Reference number: A90433; MUID:80088230; PMID:518845
 A;Contents: annotation; cross-linking acceptor sites
 R; Henschel, A.; Lottspeich, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A;Title: Covalent structure of fibrinogen.
 A;Reference number: A90337; MUID:83254370; PMID:6575689
 A;Contents: annotation; review, disulfide bonds
 R; Itarte, E.; Plaza, M.; Gusch, M.D.; Marios, C.
 Biochem. Biophys. Res. Commun. 117, 631-636, 1983
 A;Title: Phosphorylation of fibrinogen by cseain kinase 1.
 A;Reference number: A90116; MUID:84104274; PMID:6318767
 A;Contents: annotation; phosphorylation
 R; Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A;Title: Fibrinogen and fibrin.
 A;Reference number: A90041; MUID:84305751; PMID:6383194
 A;Contents: annotation; review, EM structure, polymerization, ligands
 R; Kimura, S.; Aoki, N.
 J. Biol. Chem. 261, 15501-15595, 1986
 A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
 A;Reference number: A92565; MUID:87057190; PMID:2877981
 A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
 R; Krishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
 Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
 A;Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of prote A;Reference number: A31261; MUID:8939031; PMID:2783136
 A;Contents: annotation; activity of cell attachment (R-G-D) motif
 R; Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13689-13676, 1990
 A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te A;Reference number: A37117; MUID:190337977; PMID:2143188
 A;Contents: annotation; hemlein cleavage site
 A;Note: hemlein, a protease from Haementeria ghilianii, the giant South American leech,
 R; Staendker, L.; Sillard, R.; Benach, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schep, Biochem. Biophys. Res. Commun. 215, 896-902, 1995
 A;Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites an A;Reference number: JC334; MUID:196027996; PMID:7488058
 A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptide C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated
 C;Comment: The alpha chain binds to 2-4 cross-links to the amino end of fibrinectin.
 C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabilizer) and between alpha chains (weaker) of different monomers.
 C;Comment: All fibrinogen chains are synthesized in the liver.
 C;Comment: See PIR4434 for the minor alternative splice form.
 C;Genetics:
 A;Gene: GDB:FGA
 A;Cross-references: GDB:119129; OMIM:134820
 C;Keywords: alternative splicing; fibrinogen; disulfide ring homology
 A;Position: 402-4028
 A;Intron: 18/3, 60/3, 122/1, 171/2
 A;Note: the list of introns is incomplete
 C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see C;Comment: The fibrinogen monomers that are polymerized into f
 C;Function: fibrinogen cleaved by thrombin yields monomers that are polymerized into f
 A;Pathway: blood coagulation
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C;Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; pi
 F;1-19/Domain: signal sequence #status predicted <SIC>
 F;20-629/Product: fibrinogen alpha chain #status experimental <AP>
 F;20-35/Product: fibrinopeptide A #status experimental <AP>
 F;36-629/Product: fibrin alpha chain #status experimental <FGA>
 F;57-185/Region: polymerization site, binding to the distal domain of the gamma chain of
 F;51-59/Region: fibrinogen disulfide ring homology <FDR>
 A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
 A;Reference number: A92225; MUID:78130085; PMID:632262

F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:47/Disulfide bonds: interchain (to beta-95) #status experimental
 F:55/Disulfide bonds: interchain (to beta-95) #status experimental
 F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
 F:68/Disulfide bonds: interchain (to beta-106) #status experimental
 F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
 F:184/Disulfide bonds: interchain (to beta-223) #status experimental
 F:288/Cross-link: isopeptide (Asn) (covalent) #status absent
 F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #status experimental
 F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status experimental
 F:461-491/Disulfide bonds: #status experimental
 F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status experimental
 F:686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.7%; Score 57; DB 2; Length 866;
 Best Local Similarity 91.7%; Pred. No. 0.033;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 24 ESDFLAEGGVR 35

RESULT 9
 D44234
 fibrinogen alpha chain precursor, extended splice form - human
 N:Contains: names: coagulation factor I
 C:Species: Homo sapiens (man)
 C:Accession: 10-Jun-1993 #sequence_revision 05-Sep-1996 #text_change 19-Jan-2001
 C:Accession: D44234; E44234
 R:Pu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redman, B.; Biochemistry 31, 11966-11972, 1992
 A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel A:Reference number: A44234; MUID:93090725; PMID:1457396
 A:Accession: D44234
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA; DNA
 A:Residues: 1-866 <FU1>
 A:Cross-references: GB:M58569; NID:9182406; PID:9182407
 A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
 A:Accession: B44234
 A:Residues: 605-866 <FU2>
 A:Note: sequence extracted from NCBI backbone (NCBIP:119917)
 C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleavage sites responsible for the formation of the soft clot.
 C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabilizer) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesised in the liver.
 C:Comment: See PIR:FGUA for the major splice form.
 C:Genetics:
 A:Gene: GDB:FGA
 A:Cross-references: GDB:119129; OMIM:134820
 A:Map Position: 4q28-4q28
 A:Introns: 18/3; 60/3; 122/1; 171/2
 A:Note: the list of introns is incomplete
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical chains in the core. Two three-chain coiled coils emerge from this core and connect it to distal domain nodes.
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into A:Pathway: blood coagulation
 C:Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 C:Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
 F:1-19/Domain: signal sequence #status predicted <SG>
 F:20-36/Domain: fibrinogen alpha chain, extended splice form #status predicted <WAT>
 F:36-863/Product: fibrinopeptide A #status experimental <AP>
 F:36-863/Product: fibrinogen alpha chain, extended splice form #status predicted <FGA>
 F:57-185/Domain: fibrinogen disulfide ring homology <FR>
 F:591-593/Domain: cell attachment (R-G-D) motif
 F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
 F:22-460/Binding site: phosphate (Ser) (covalent) #status experimental

fibrinogen alpha chain - dog (fragment)
 C;Species: *Canis lupus familiaris* (dog)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996

R;Birken, S.; Wilner, G.D.; Canfield, R.B.
 Thromb. Res. 7, 599-610, 1975
 A;Title: Studies of the structure of canine fibrinogen.
 A;Reference number: A94308; PMID:1198347

A;Accession: A94308
 A;Molecule type: protein

A;Residues: 1-28 <BLO>

R;Blomhaeck, B.; Blomhaeck, M.; Groendahl, N.J.
 Acta Chem. Scand. 19, 1789-1791, 1965

A;Title: Studies on fibrinopeptides from mammals.
 A;Reference number: A03118

A;Accession: A03118
 A;Molecule type: protein

A;Residues: 1-16 <BLO>

R;Osahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
 Biochem. Biophys. Res. Commun. 14, 555-558, 1964

A;Reference number: A37511
 A;Molecule type: protein

A;Residues: 1', D, 3', EGKQ', 8-16 <OSB>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C;Keywords: blood coagulation; liver; phosphoprotein; plasma

F;1'-6/Product: fibrinopeptide A #status experimental <APT>

F;Binding site: phosphate (Ser) (covalent) (partial) #status experimental
 Query Match 78.5%; Score 51; DB 2; Length 28;

Best Local Similarity 75.0%; Pred. No. 0.016;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 5 EGEFTAEGGGR 16

RESULT 13
 B29501

fibrinopeptide A - pig

C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000

C;Accession: B29501
 R;Blomhaeck, B.; Blomhaeck, M.; Hann, C.
 unpublished results, cited by Blomhaeck, B., and Blomhaeck, M., in Chemotaxonomy and Ser

A;Reference number: A29501
 A;Accession: B29501
 A;Molecule type: protein

A;Residues: 1-17 <BLO>

R;Blomhaeck, B.; Blomhaeck, M.; Groendahl, N.J.
 Acta Chem. Scand. 19, 1789-1791, 1965

A;Title: Studies on fibrinopeptides from mammals.
 A;Reference number: A03118

C;Superfamily: fibrinogen beta chain; fibrinogen disulfide ring homology; fibrinogen gamma chain; fibrinogen disulfide ring homology

Query Match 75.4%; Score 49; DB 2; Length 17;

Best Local Similarity 75.0%; Pred. No. 0.022;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 6 KGBFLAEGGGR 17

RESULT 14
 I29501
 fibrinopeptide A - kangaroo
 C;Species: *Macropus* sp. (kangaroo)
 C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
 C;Accession: I29501
 R;Blomhaeck, B.; Blomhaeck, M.; Hann, C.

unpublished results, cited by Blomhaeck, B., and Blomhaeck, M., in Chemotaxonomy and Ser

A;Reference number: A29501
 A;Accession: I29501
 A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BLO>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 73.8%; Score 48; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 0.029;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
 Db 4 EGFPIAEGGGR 15

RESULT 15
 B29501

fibrinopeptide A - European moose

C;Species: *Alces alces* (European moose, elk)

C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000

C;Accession: B29501
 R;Blomhaeck, B.; Blomhaeck, M.; Hann, C.
 unpublished results, cited by Blomhaeck, B., and Blomhaeck, M., in Chemotaxonomy and Ser

A;Reference number: A29501
 A;Accession: B29501
 A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <BLO>

C;Superfamily: fibrinogen beta chain; fibrinogen gamma chain; fibrinogen disulfide ring homology

Query Match 73.0%; Score 40; DB 2; Length 19;

Best Local Similarity 90.0%; Pred. No. 0.037;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGR 13
 Db 10 EFLAEGGGR 19

Search completed: February 10, 2003, 16:07:25

Job time : 18 secs

THIS PAGE BLANK (USPTO)

Scoring table:	BLOSUM62	Gapop:	10.0	Gapext:	0.5
Searched:	112892 seqs, 41476328 residues	Total number of hits satisfying chosen parameters:	112892	Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Post-processing:	Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries	SUMMARIES	
Database :	SwissProt_40.4	%		Description	
Result No.	Score	Query Match	Length	DB ID	
1	57	87.7	16	1	P12803 macaca fasciularis
2	57	87.7	19	1	P14446 cervus elaphus
3	57	87.7	866	1	P02671 homo sapiens
4	56	86.2	16	1	P14535 ceratotherium simum
5	54	83.1	16	1	P14536 tapiro tapiro
6	53	81.5	16	1	P14453 hylobates lar
7	53	81.5	18	1	P14448 camelus dromedarius
8	53	81.5	19	1	P14441 bison bonasus
9	53	81.5	19	1	P14447 cervus nivalis
10	51	78.5	16	1	P14450 felis silvestris
11	51	78.5	28	1	P02673 canis familiaris
12	49	75.4	17	1	P14460 sus scrofa
13	49	75.4	18	1	P14454 lama glama
14	48	73.8	15	1	P14463 synodus caninus
15	48	73.8	16	1	P14449 equus asinus
16	48	73.8	16	1	P14455 mandrillus leucophaeus
17	48	73.8	16	1	P14459 odcoileus hemionus
18	48	73.8	19	1	P14442 bubalus bubalis
19	48	73.8	19	1	P14451 ovis aries
20	48	73.8	596	1	P02672 bos taurus
21	47	72.3	14	1	P14452 equus caballus
22	45	69.2	19	1	P14457 muntiacus muntjak
23	40	61.5	15	1	P12801 anas platyrhynchos
24	40	61.5	1696	1	P14451 brachyrhynchus brachyrhynchus
25	39	60.0	13	1	P14445 cavia porcellus
26	39	60.0	236	1	P02673 equus caballus
27	39	60.0	271	1	P29808 pseudomonas aeruginosa
28	38	58.5	611	1	P04813 pseudomonas aeruginosa
29	38	58.5	742	1	P14457 sunia sunia
30	37	56.9	19	1	P14452 rangifer tarandus
31	37	56.9	413	1	P06187 glycine maxima
32	37	56.9	415	1	P50218 nicotiana tabacum
33	37	56.9	416	1	P50217 solanum tuberosum

DR	PIR; B24180; B24180.	
DR	A28854; A28854.	
DR	PIR; B28854; B28854.	
DR	PIR; C28854; C28854.	
KW	Blood coagulation.	
FT	BPETIDE 1 16	FIBRINOPEPTIDE A.
FT	NON TER 16 16	
SQ	SEQUENCE 16 AA; 1551 MW;	49E8CBB3EA04DD3 CRC64;
Query Match	Best Local Similarity 91.7%; Matches 11; Conservative 0; Mismatches 1; Indels 0;	Score 57; DB 1; Length 16; Pred. No. 0.00034;
Qy	2 EDDFLAEGGGV 13	
Db	5 EGDFLAEGGGV 16	
RESULT 2		
ID	FBBA_CEREL	STANDARD;
AC	P14476.	PRT; 19 AA.
DT	01-JAN-1990 (Rel. 13. Created)	
DT	01-JAN-1990 (Rel. 13. Last sequence update)	
DT	15-JUN-2002 (Rel. 41. Last annotation update)	
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).	
DE	GN FGA.	
OS	Cervus elaphus (Red deer), and	
OS	Cervus elaphus nelsoni (American elk)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea; Cervidae; Cervinae; Cervus;	
OC	NCBI TaxID:9860, 9864;	
RN	SEQUENCE.	
RC	SPECIES=C.e.elaphus;	
RA	Blobback B., Blomback M., Grondahl N.J.;	
RT	"Studies on fibrinopeptides from mammals.";	
RL	Acta Chem. Scand. 19:1789-1791(1965).	
RN	SEQUENCE.	
RC	SPECIES=C.e.nelsoni;	
RA	Mross G.A., Doolittle R.F.;	
RT	"Amino acid sequence studies on artiodactyl fibrinopeptides.";	
RL	Arch. Biochem. Biophys. 122:674-684(1967).	
CC	- I - FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.	
CC	- I - SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	
CC	- I - MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.	
KW	Blood coagulation; Plasma.	FIBRINOPEPTIDE A.
FT	PEPTIDE 1 19	
FT	NON TER 19 19	
SQ	SEQUENCE 19 AA; 1808 MW;	9BA54C2687B59C5 CRC64;
Query Match	Best Local Similarity 84.6%; Matches 11; Conservative 1; Mismatches 1; Indels 0;	Score 57; DB 1; Length 19; Pred. No. 0.00041;
Qy	1 SESDFLAEGGGV 13	
Db	7 ASSDFLAEGGGV 19	
RESULT 3		
ID	FBBA_HUMAN	STANDARD;
AC	P02671; Q9BX62; Q9UCH2;	PRT; 866 AA.
DT	21-JUL-1986 (Rel. 01, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Fibrinogen alpha/beta chain precursor [Contains: Fibrinopeptide A].	
GN	FGA.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC	NCBI_TaxID:9606;	
RN	[1] _TAXID=9606;	
RP	SEQUENCE FROM N.A. (ALPHA-E FORM).	
RX	Medline=93090725; PubMed=1457396;	
RA	Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J., Roy S.N., Redman C.M., Grieninger G.;	
RA	"Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel exon conferring marked homology to beta and gamma subunits.";	
RT	Biochemistry 31:11968-11972 (1992).	
RN	[2]	
RP	SEQUENCE FROM N.A. (ALPHA-E FORM).	
RA	Chung D.W., Grieninger G.;	
RT	"Fibrinogen DNA and protein sequences";	
RL	(In) Ebert R.F. (eds.); CRC Press B.	
RL	Index of variant human fibrinogens, pp.13-24.	
RL	Boca Raton (1994).	
RN	[3]	
RP	SEQUENCE FROM N.A. (ALPHA-E, ALPHA), AND VARIANTS VAL-6; ALA-331 AND ALA-456.	
RA	Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Riedler M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Chung D.W., Harris J.B., Davie E.W.;	
RA	Nicholson D.A.;	
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.	
RN	[4]	
RP	SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).	
RC	TISSUE=Liver.	
RX	Medline=91344740; PubMed=2102623;	
RA	Chung D.W., Harris J.B., Davie E.W.;	
RT	"Nucleotide sequences of the three genes coding for human fibrinogen";	
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.	
RN	[5]	
RP	SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).	
RX	Medline=91344740; PubMed=2102623;	
RA	Kant J.A., Lord S.T., Crabtree G.R.;	
RT	"Partial mRNA sequences for human A alpha, B beta, and gamma fibrinogen chains: evolutionary and functional implications.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957 (1993).	
RN	[6]	
RP	SEQUENCE FROM N.A. (ALPHA FORM).	
RA	Medline=93247396; PubMed=6575389;	
RA	Kant J.A., Lord S.T., Crabtree G.R.;	
RT	"Partial mRNA sequences for human A alpha, B beta, and gamma fibrinogen chains: evolutionary and functional implications.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957 (1993).	
RN	[7]	
RP	SEQUENCE OF 1-629 FROM N.A.	
RA	Medline=93283432; PubMed=6688355;	
RA	Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;	
RT	"Characterization of a complementary deoxyribonucleic acid coding for the alpha chain of human fibrinogen.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957 (1993).	
RL	Biochemistry 22:3237-3244 (1983).	
RN	[8]	
RP	SEQUENCE OF 20-629.	
RA	"Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural variants.";	
RT	(In) Peeters H. (eds.); Pergamon Press, Oxford (1980).	
RL	Provides of the biological fluids, Proc. 28th colloquium, pp.51-56,	
RN	[9]	
RP	SEQUENCE OF 20-629, AND DISULFIDE BONDS.	
RA	Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;	
RT	"Amino acid sequence studies on the alpha chain of human fibrinogen. Overlapping sequences providing the complete sequence.";	
RL	Biochemistry 18:5410-5416 (1979).	
RN	[9]	
RP	SEQUENCE OF 110-156 FROM N.A.	
RX	Medline=94069777; PubMed=6689067;	
RA	Imam A.M., Eaton M.A., Williamson R., Humphries S.;	
RT	"Isolation and characterisation of cDNA clones for the A alpha- and gamma-chains of human fibrinogen.";	
RT		

RL Nucleic Acids Res. 11:7427-7434 (1983).
 RN [10] RX MEDLINE=983556117; PubMed=9689040;
 RP Spraggan G., Applegate D., Everse S.J., Zhang J.Z., Verapandian L.,
 RA Redman C., Doolittle R.F., Grieninger G.;
 RA "Sequence of 605-644 from N.A. (Alpha Form)."
 RX MEDLINE=8254384; PubMed=6575700;
 RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
 RT "Cloning of fibrinogen genes and their cDNA.";
 RL Ann. N.Y. Acad. Sci. 408:449-456 (1983).
 RN [11] RX X-RAY CRYSTALLOGRAPHY.
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=9175089; PubMed=10074346;
 RA Everse S.J., Spraggan G., Verapandian L., Doolittle R.F.;
 RT "Studies on fibrinopeptides from primates.";
 RL "Crystal structure of a recombinant alphaEC domain from human
 fibrinogen-420.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104 (1998).
 RN [12] RX X-RAY CRYSTALLOGRAPHY.
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=92346680; PubMed=1634621;
 RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy J.,
 RA Perez-Requejo J.L., Matsuda M.;
 RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
 characterized by the replacement of A alpha proline-18 by leucine.";
 RL Biochemistry 38:2941-2946 (1999).
 RN [23] RX VARIANT KYOTO-2.
 RP VARIANT KYOTO-2.
 RX MEDLINE=1300048; PubMed=2070049;
 RA Yoshiida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
 RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
 characterized by the replacement of A alpha proline-18 by leucine.";
 RL Blood 78:149-153 (1991).
 RN [24] RX VARIANT LIMA.
 RP VARIANT LIMA.
 RX MEDLINE=12346680; PubMed=16126018;
 RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA de Bosch N., Arocha-Pinango C.L., Carvajal Z., Ojeda A.,
 RA Perez-Requejo J.L., Matsuda M.;
 RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A
 alpha-arginine-141 to serine substitution associated with extra
 RT N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel
 formation but normal fibrin-facilitated plasminogen activation
 RT catalyzed by tissue-type plasminogen activator.";
 RL J. Clin. Invest. 90:67-76 (1992).
 RN [25] RX VARIANT CARACAS-2.
 RP VARIANT CARACAS-2.
 RX MEDLINE=12346680; PubMed=16126018;
 RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA Takahashi N., de Bosch N., Arocha-Pinango C.L., Carvajal Z., Ojeda A.,
 RA Perez-Requejo J.L., Matsuda M.;
 RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a
 dysfibrinogen, fibrinogen Caracas II, characterized by impaired
 RT fibrin gel formation.";
 RL J. Biol. Chem. 266:11575-11581 (1991).
 RN [26] RX VARIANT DUSART.
 RP VARIANT DUSART.
 RX MEDLINE=9332289; PubMed=8473507;
 RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
 RA Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
 RA Caen J.P.;
 RA "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and
 RT its association with abnormal fibrin polymerization and
 RT thrombophilia.";
 RT [17] RX PHOSPHORYLATION.
 RP PHOSPHORYLATION.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229 (1984).
 RN [18] RX CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
 RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
 RX MEDLINE=87057190; PubMed=28777981;
 RA Kimura S., Aoki N.;
 RA "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
 RL J. Biol. Chem. 261:15591-15595 (1986).
 RN [19] RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
 RX MEDLINE=9218459; PubMed=6318767;
 RA Itarte E., Plana M., Guasch M.D., Martos C.;
 RA "Phosphorylation of fibrinogen by casein kinase 1.";
 RL Biochem. Biophys. Res. Commun. 117:631-636 (1983).
 RN [20] RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
 RX MEDLINE=9292395; PubMed=9628725;
 RA Everse S.J., Spraggan G., Verapandian L., Riley M., Doolittle R.F.;
 RT "The structure of residues 7-16 of the A alpha-chain of human
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 RL J. Biol. Chem. 267:7911-7920 (1992).
 RN [21] RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.

Query Match 87.7%; Score 57; DB 1; Length 866;
 Best Local Similarity 91.7%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDPLAEGGVR 13
 Db 24 EGDPLAEGGVR 35

RESULT 4
 FIBA_CERSI STANDARD;
 AC P14535;
 ID FIBA_CERSI
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibropetide A] (Fragment).
 FN Cera-totherium simum (White rhinoceros) (Square-lipped rhinoceros).
 OS Ceratotherium simum (White rhinoceros); Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Buharyota; Metazoa; Chordata; Craniata; Vertebrata; Rhinocerotidae; Ceratotherium.
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.

OX	NCBI_TaxID=9807;	/	AC P14453;	DT 01-JAN-1990 (Rel. 13, Created)
RN	[1]		DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 01-JUN-2002 (Rel. 41, Last annotation update)
RP	O'Neil P.B.; Doolittle R.F.;		RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RA	O'Neil P.B.; Doolittle R.F.;		RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RR			RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL			RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
CC	-1- FUNCTION: FIBRINOCEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT		CC -1- FUNCTION: FIBRINOCEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT	CC -1- FUNCTION: FIBRINOCEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC	POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET		CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET	CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC	AGGREGATION.		CC AGGREGATION.	CC AGGREGATION.
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS		CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS	CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC	(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.		CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY		CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY	CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC	THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA		CC THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA	CC THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA
CC	CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES		CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES	CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.		CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.	CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW	Blood coagulation; Plasma.		KW Blood coagulation; Plasma.	KW Blood coagulation; Plasma.
FT	PEPTIDE 1	16	FT PEPTIDE 1	16
FT	NON TER 16	16	FT NON TER 16	16
SQ	SEQUENCE 16 AA; 1639 MW;	0958CBB6293F4C81 CRC64;	SQ SEQUENCE 16 AA; 1639 MW;	SQ SEQUENCE 16 AA; 1639 MW;
Qy	1 SESDFLAEGGGV 13		Qy 1 SESDFLAEGGGV 13	Qy 1 SESDFLAEGGGV 13
Db	4 TEQDFLAEGGGV 16		Db 4 TEQDFLAEGGGV 16	Db 5 EGEEFLAEGGGV 16
RESULT 5	FIBA_TAPTE		RESULT 7	FIBA_CAMDR
ID	FIBA_TAPTE	STANDARD;	ID	FIBA_CAMDR
AC	P14536;	PRT; 16 AA.	AC	P1444;
DT	01-JAN-1990 (Rel. 13, Created)		DT	01-JAN-1990 (Rel. 13, Created)
DT	01-JAN-1990 (Rel. 13, Last sequence update)		DT	01-JAN-1990 (Rel. 13, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)		DT	15-JUN-2002 (Rel. 41, Last annotation update)
CC	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).		CC Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).	CC Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN	FGA.		GN FGA.	GN FGA.
OS	Tapirus terrestris (Lowland tapir) (Brazilian tapir).		OS Camelus dromedarius (Dromedary) (Arabian camel).	OS Camelus dromedarius (Dromedary) (Arabian camel).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Tylopoda; Camelidae; Camelus.	OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OC	Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.		OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.	OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX	NCBI_TaxID=9801;		OX NCBI_TaxID=9801;	OX NCBI_TaxID=9801;
RN	RP	SEQUENCE.	RN RP	SEQUENCE.
RA	O'Neil P.B.; Doolittle R.F.;	"Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RA Doolittle R.F.; Schubert D.; Schwartz S.A.;	RA Doolittle R.F.; Schubert D.; Schwartz S.A.;
RT	O'Neil P.B.; Doolittle R.F.;	"Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.	RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RL	O'Neil P.B.; Doolittle R.F.;	"Mammalian phylogeny based on fibrinopeptide amino acid sequences.";	RL Dromedary camel, mule deer, and cape buffalo.";	RL Dromedary camel, mule deer, and cape buffalo.";
CC	-1- FUNCTION: FIBRINOCEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT		CC Arch. Bioophys. 118:456-467(1967).	CC Arch. Bioophys. 118:456-467(1967).
CC	POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET		CC -1- FUNCTION: FIBRINOCEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT	CC -1- FUNCTION: FIBRINOCEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC	AGGREGATION.		CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET	CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS		CC AGGREGATION.	CC AGGREGATION.
CC	(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.		CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS	CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY		CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC	THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA		CC THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA	CC THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA
CC	CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES		CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES	CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
KW	Blood coagulation; Plasma.		KW Blood coagulation; Plasma.	KW Blood coagulation; Plasma.
FT	PEPTIDE 1	16	FT PEPTIDE 1	16
FT	NON TER 16	16	FT NON TER 16	16
SQ	SEQUENCE 16 AA; 1622 MW;	48598B6292F4030 CRC64;	SQ SEQUENCE 16 AA; 1622 MW;	SQ SEQUENCE 16 AA; 1622 MW;
Qy	1 SESDFLAEGGGV 13		Qy 1 SESDFLAEGGGV 13	Qy 1 SESDFLAEGGGV 13
Db	4 TEQDFLAEGGGV 16		Db 4 TEQDFLAEGGGV 16	Db 5 EGEEFLAEGGGV 16
RESULT 6	FIBA_HYLLA		RESULT 6	FIBRINOPEPTIDE A.
ID	FIBA_HYLLA	STANDARD;	ID FIBA_HYLLA	STANDARD;
PRT;	16 AA.	PRT; 16 AA.	PRT; 16 AA.	PRT; 16 AA.

Query Match	Score 81.5%; Best Local Similarity 83.3%; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 EGFELAEGGGVR 18	Score 53; DB 1; Length 18; Pred. No. 0.002; Prd. No. 0.002; Best Local Similarity 83.3%; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 EGFELAEGGGVR 18	Score 53; DB 1; Length 18; Pred. No. 0.002; Prd. No. 0.002; Best Local Similarity 83.3%; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 EGFELAEGGGVR 18
RESULT 8			
FIBA_BISBO	STANDARD; PRT; 19 AA.	STANDARD; PRT; 19 AA.	STANDARD; PRT; 19 AA.
P14471; DT 01-JAN-1990 (Rel. 13, Created) DT 01-JAN-1990 (Rel. 13, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update)	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.
OS BISON	Bison bonasus (European bison)	Bison bonasus (European bison)	Bison bonasus (European bison)
OC Mammalia	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bison.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bison.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bison.
NCBI_TaxID:9902;	[1]	[1]	[1]
RN P14471; RA Blomback B., Blomback M., Grondahl N.J.; RT "Studies on Fibrinopeptides from mammals."; Acta Chem. Scand. 19:1789-1791 (1965).	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC CC CC CC CC CC	Fibrinogen, which cleaves fibrinopeptides A and B from alpha & beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.	Fibrinopeptide A.	Fibrinopeptide A.
CC CC CC CC CC CC	Blood coagulation; Plasma.	PEPTIDE 1 19	SEQUENCE 19 AA; 1836 MW; 9BA55A0F73B59C5 CRC64;
CC CC CC CC CC CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.	SEQUENCE 19 AA; 1836 MW; 9BA55A0F73B59C5 CRC64;	SEQUENCE 19 AA; 1836 MW; 9BA55A0F73B59C5 CRC64;
CC CC CC CC CC CC	Blood coagulation; Plasma.	Score 81.5%; Best Local Similarity 76.9%; Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Sequence 1 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 19	Score 53; DB 1; Length 19; Pred. No. 0.0021; Prd. No. 0.0021; Best Local Similarity 76.9%; Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Sequence 1 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 19
CC CC CC CC CC CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.	Score 53; DB 1; Length 19; Pred. No. 0.0021; Prd. No. 0.0021; Best Local Similarity 76.9%; Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Sequence 1 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 19	Score 53; DB 1; Length 19; Pred. No. 0.0021; Prd. No. 0.0021; Best Local Similarity 76.9%; Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Sequence 1 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 19
RESULT 9			
FIBA_CERNI	STANDARD; PRT; 19 AA.	STANDARD; PRT; 19 AA.	STANDARD; PRT; 19 AA.
P14471; DT 01-JAN-1990 (Rel. 13, Created) DT 01-JAN-1990 (Rel. 13, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update)	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.
OS Cervus	Cervus nippon (Sika deer).	Cervus nippon (Sika deer).	Cervus nippon (Sika deer).
OC Mammalia	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea; Cervidae; Cervinae; Cervus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea; Cervidae; Cervinae; Cervus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea; Cervidae; Cervinae; Cervus.
NCBI_TaxID:9063;	[1]	[1]	[1]
RN P14471; RA Blomback B., Blomback M., Grondahl N.J., Holmberg E.; RT "Structure of Fibrinopeptides-its relation to enzyme specificity and phylogeny and classification of species."; Ark. Kemi 25:411-428 (1966).	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
CC CC CC CC CC CC	SEQUENCE 11	SEQUENCE 11	SEQUENCE 11
CC CC CC CC CC CC	FIBA_CANFA	FIBA_CANFA	FIBA_CANFA
CC CC CC CC CC CC	STANDARD; PRT; 28 AA.	STANDARD; PRT; 28 AA.	STANDARD; PRT; 28 AA.
CC CC CC CC CC CC	AC P02673; P14464; DT 01-JUL-1986 (Rel. 01, Created)	AC P02673; P14464; DT 01-JUL-1986 (Rel. 01, Created)	AC P02673; P14464; DT 01-JUL-1986 (Rel. 01, Created)
CC CC CC CC CC CC	Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 16	Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 16	Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 16
CC CC CC CC CC CC	Blood coagulation; Plasma.	Blood coagulation; Plasma.	Blood coagulation; Plasma.
CC CC CC CC CC CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC CC CC CC CC CC	PEPTIDE 1 16	PEPTIDE 1 16	PEPTIDE 1 16
CC CC CC CC CC CC	SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;	SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;	SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;
CC CC CC CC CC CC	Score 78.5%; Best Local Similarity 75.0%; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 16	Score 51; DB 1; Length 16; Prd. No. 0.004; Prd. No. 0.004; Best Local Similarity 75.0%; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 16	Score 51; DB 1; Length 16; Prd. No. 0.004; Prd. No. 0.004; Best Local Similarity 75.0%; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Sequence 2 ESDFLAEGGGVR 13 7 ASDFLAEGGGVR 16
CC CC CC CC CC CC	FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.	FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.	FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
CC CC CC CC CC CC	RESULTS 12	RESULTS 12	RESULTS 12
CC CC CC CC CC CC	FIBA_CANFA	FIBA_CANFA	FIBA_CANFA
CC CC CC CC CC CC	STANDARD; PRT; 28 AA.	STANDARD; PRT; 28 AA.	STANDARD; PRT; 28 AA.
CC CC CC CC CC CC	AC P02673; P14464; DT 01-NOV-1990 (Rel. 01, Last sequence update)	AC P02673; P14464; DT 01-NOV-1990 (Rel. 01, Last sequence update)	AC P02673; P14464; DT 01-NOV-1990 (Rel. 01, Last sequence update)
CC CC CC CC CC CC	DE Fabrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.	DE Fabrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.	DE Fabrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). FGA.
CC CC CC CC CC CC	OS Canis familiaris (Dog); and Vulpes vulpes (Red Fox).	OS Canis familiaris (Dog); and Vulpes vulpes (Red Fox).	OS Canis familiaris (Dog); and Vulpes vulpes (Red Fox).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID:9615, 9622 ;

RN [1] SEQUENCE.

RC SPECIES=C.familiaris;

RP MEDLINE=76081726; PubMed=1198547;

RX Birken S., Wilner G.D., Canfield R.E.; fibrinogen.;"

RT "Studies on the structure of canine fibrinogen." ;

RL Thromb. Res. 7:599-610(1975).

RN [2] SEQUENCE OF 1-16.

RC SPECIES=C.familiaris, and V.vulpes;

RA Blomback B., Blomback M., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals." ;

RL Acta Chem. Scand. 19:1789-1791(1965).

RN [3] SEQUENCE OF 1-16.

RC SPECIES=C.familiaris;

RP MEDLINE=6620594; PubMed=5836555;

RA Osbahr A.J. Jr., Coiman R.W., Laki K., Gladner J.A.;

RT "The nature of the peptides released from canine fibrinogen." ;

RL Biochem. Biophys. Res. Commun. 14:555-558(1964).

CC -!- FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA) LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -!- MISCELLANEOUS: CONVERSION OF FIBRINogen TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINopeptides A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

PIR: A03118; A05296.

DR PIR: A05296; A05296.

KW Blood coagulation; Plasma; Phosphorylation.

FT PEPTIDE 1 16 FIBRINopeptide A.

FT MOD RES 3 3 PHOSPHORYLATION (IN SOME MOLECULES) .

FT CONFLICT 2 2 N -> D (IN REF. 2).

FT CONFLICT 4 7 KEGE -> EGKQ (IN REF. 2).

FT NON TER 28 28 09DCD3F923BFEBD2 CRC64;

SQ SEQUENCE 28 AA; 2958 MW; 09DCD3F923BFEBD2 CRC64;

RESULT 12

Query Match Best Local Similarity 78.5%; Score 51; DB 1; Length 28; Matches 9; Conservative 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13

Db 5 EGEFLAEGGGVR 16

PIB_A_PIG STANDARD; PRT; 17 AA.

AC P14460-0

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DB Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

GN PGA.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.

NCBI_TaxID=9823;

RN [1] SEQUENCE.

RA Blomback B., Blomback M., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals." ;

RL Acta Chem. Scand. 19:1789-1791(1965).

CC -!- FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS, WHICH CLEAVES FIBRINopeptides A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

PIR: A05296; A05296.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 18 FIBRINopeptide A.

FT NON TER 18 18 2444487B857F4CC6 CRC64;

SQ SEQUENCE 18 AA; 1834 MW; 2444487B857F4CC6 CRC64;

Query Match Best Local Similarity 75.4%; Score 49; DB 1; Length 17; Matches 9; Conservative 2; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13

Db 7 KGFLAEGGGVR 18

RESULT 14

PIB_A_SYNCA STANDARD; PRT; 15 AA.

AC P14463;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Syncerus caffer (Cape buffalo).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Bovidae; Syncerus.
 OC Bovidae; Bovinae; Syncerus.
 NCBI_TaxID=9970;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=67209145; PubMed=6033721;
 RA Doolittle R.F., Schubert D., Schwartz S.A.,
 "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
 Dromedary camel, mule deer, and cape buffalo.";
 RL Arch. Biochem. Biophys. 118:456-467 (1967).
 CC -!- FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINogen TO FIBRIN IS TRIGGERED BY
 THROMBIN, WHICH CLEAVES FIBRINopeptides A AND B FROM ALPHA & BETA
 CHAINS, AND THUS EXPOSES THE N-TERMINAL POLIMERIZATION SITES
 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
 FT NON_TER 15 15 MW; 4E998EA5F0B41CC6 CRC64;
 SQ SEQUENCE 15 AA; 4E998EA5F0B41CC6 CRC64;

Query Match Score 48; DB 1; Length 15;
 Best Local Similarity 90.0%; Pred. No. 0.013;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGVR 13
 Db 5 EFLAEGGVR 16

RESULT 15
 FIBA_EQUAS
 ID FIBA_EQUAS STANDARD PRT; 16 AA.
 AC P14439;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Equus asinus (Donkey).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE.
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791 (1955).
 CC -!- FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINogen TO FIBRIN IS TRIGGERED BY
 THROMBIN, WHICH CLEAVES FIBRINopeptides A AND B FROM ALPHA & BETA
 CHAINS, AND THUS EXPOSES THE N-TERMINAL POLIMERIZATION SITES
 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16 MW; 095988BB63C2A5957 CRC64;
 SQ SEQUENCE 16 AA; 1696 MW; 095988BB63C2A5957 CRC64;

Query Match Score 48; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.014;

THIS PAGE BLANK (USPTO)

Run on:	February 10, 2003, 15:57:51 ; Search time 92 Seconds (without alignments)
Title:	US-09-845-729-1
Perfect score:	65
Sequence:	1 SESDFAEQQGVR 13
Scoring table:	BLOSUM62
Gapop 10.0 , Gapext 0.5	
Searched:	671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters:	671580
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
Database :	SPTREMBL_1.1*
	1: sp_archea:*
	2: sp_bacteria:*
	3: sp_fungi:*
	4: sp_human:*
	5: sp_invertebrate:*
	6: sp_mammal:*
	7: sp_mhc:*
	8: sp_organelle:*
	9: sp_phage:*
	10: sp_plant:*
	11: sp_rabbit:*
	12: sp_virus:*
	13: sp_vertebrate:*
	14: sp_unclassified:*
	15: sp_virus:*
	16: sp_bacteriap:*
	17: sp_archeap:*
ALIGNMENTS	
RESULT 1	
Q8WW76	PRELIMINARY;
AC Q8WW76;	
ID Q8WW76;	
DT 01-MAR-2002 (TREMBLrel. 20, Created)	
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Similar to fibrinogen, A alpha polypeptide.	
OS Homo sapiens (Human)	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC NCBITaxonID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=LIVER;	
RA Strausberg R.;	
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.	
DR BCO20744; AAH2074.1;	
SQ SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;	
Query Match Score 57; DB 4; Length 218;	
Best Local Similarity 91.7%; Pred. No. 0.033;	
Matches 11; Conservative 0; Mismatches 1; Indels 0;	
RESULT 2	
Q8WW76 homo sapien	
Q99147 mus musculus	
Q88299 oryza sativa	
Q87255 tetrahymena	
Q9apx1 pseudomonas	
Q9wm6 staphylococ	
Q8w15 lapemis har	
Q9ug5 drosophila	
Q9873 rhizobium 1	
Q9p815 botryosphaeriales	
Q9F7D5 salmonella	
Q86k4 salmonella	
Q9484 salmonella	
Q53481 mycobacteri	
Q9h81 arabidopsis	
Q94074	
Mus musculus (Mouse).	
Result No. Score Query Match Length DB ID Description	
- - - - -	
1 56 87.7 Q8WW76	
2 46 70.8 557 11 Q99K47	
3 43 66.2 260 10 Q8S2N9	
4 41 63.1 242 5 Q8T925	
5 41 63.1 552 2 Q9APX1	
6 40 61.5 280 16 Q99WM6	
7 40 61.5 630 13 Q8UW15	
8 40 61.5 852 5 Q9U4G5	
9 39 60.0 89 16 Q98F73	
10 39 60.0 171 3 Q9F7D5	
11 39 60.0 186 2 Q9873	
12 39 60.0 245 16 Q8Z6K4	
13 39 60.0 245 16 Q9Z4S4	
14 39 60.0 324 16 Q53481	
15 39 60.0 465 10 Q9LH81	
16 39 60.0 465 10 Q94074	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	56	87.7	218	4	Q8WW76		
2	46	70.8	557	11	Q99K47		
3	43	66.2	260	10	Q8S2N9		
4	41	63.1	242	5	Q8T925		
5	41	63.1	552	2	Q9APX1		
6	40	61.5	280	16	Q99WM6		
7	40	61.5	630	13	Q8UW15		
8	40	61.5	852	5	Q9U4G5		
9	39	60.0	89	16	Q98F73		
10	39	60.0	171	3	Q9F7D5		
11	39	60.0	186	2	Q9873		
12	39	60.0	245	16	Q8Z6K4		
13	39	60.0	245	16	Q9Z4S4		
14	39	60.0	324	16	Q53481		
15	39	60.0	465	10	Q9LH81		
16	39	60.0	465	10	Q94074		

OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR	EMBL; AY075152; Score 41; DB 5; Length 242;
OC	NCBI_TaxID=10090;	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RN	[1]	Query Match	Query Match
RA	Strausberg R.;	Best Local Similarity 63.1%; Score 41; DB 5;	Best Local Similarity 63.1%; Score 41; DB 5;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;	Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DR	DR	Qy	Qy
DR	HSSP: P02671; 1FZA.	1 SESDFLAEGGVR 10	1 SESDFLAEGGVR 10
DR	NGD; MGI:1316726; FgA.	Db	77 SKNDPIAEQQ 86
SQ	SEQUENCE 557 AA; 61325 MW; C47F946D1BA432DE CRC64;		
<hr/>			
RESULT 5		RESULT 5	RESULT 5
Q8S2N9	PRELIMINARY;	Q9APX1	Q9APX1
AC	Q8S2N9;	ID	ID
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Q9APX1;	PRELIMINARY;
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	Q9APX1;	PRELIMINARY;
Qy	2 ESDFLEAGGGVR 13	AC	AC
Db	25 KGEFLSEGGGVR 36	RN	[1]
<hr/>			
RESULT 3		RESULT 3	RESULT 3
Q8S2N9	PRELIMINARY;	Q9APX1	Q9APX1
AC	Q8S2N9;	ID	ID
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Q9APX1;	PRELIMINARY;
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	Q9APX1;	PRELIMINARY;
Qy	OS Oryza sativa (Japonica cultivar-group).	AC	AC
Db	OC Spermatophyta; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidea; Orzyeae; Orzyza.	RN	RN
RN	[1]	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	RC	Qy	Qy
RA	RA	1 SESDFLAEGGVR 13	1 SESDFLAEGGVR 13
RT	RT	Db	Db
RT	"Oryza sativa nippobare (GA3) genomic DNA, chromosome 1, BAC clone B1066G12.1; Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	58 STADFYSAAGGIR 70	58 STADFYSAAGGIR 70
RL	DR EMBL; AP003201; BAB89442.1; -		
DR	SEQUENCE 260 AA; 29524 MW; 40929C6C486F0F06 CRC64;		
SQ			
<hr/>			
RESULT 9		RESULT 9	RESULT 9
Q8T925	PRELIMINARY;	Q99WM6	Q99WM6
AC	Q8T925;	ID	ID
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Q99WM6;	PRELIMINARY;
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	Q99WM6;	PRELIMINARY;
Q8T925	SEQUENCE FROM N.A.	AC	AC
AC	AC	RN	RN
DT	01-JUN-2002 (TREMBLrel. 21, Created)	SEQUENCES=S.aureus (strain Mu50), and S.aureus (strain N315);	SEQUENCES=S.aureus (strain Mu50), and S.aureus (strain N315);
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	RX	RX
Q8T925	SEQUENCE FROM N.A.	RA	RA
AC	AC	RX	RA
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	RN	RN
Q8T925	SEQUENCE FROM N.A.	RA	RA
AC	AC	RN	RA
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Maruyama A., Murakami H., Hosoyama A.,	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Maruyama A., Murakami H., Hosoyama A.,
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	RN	RA
Q8T925	SEQUENCE FROM N.A.	RA	Mizutani K., Takahashi N. K., Goto T., Inoue R.-I., Kaito C.,
AC	AC	RA	RA
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Kanemizu K., Hirashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,	Kanemizu K., Hirashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	RN	RA
Q8T925	SEQUENCE FROM N.A.	RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
AC	AC	RA	
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC	AC		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
Q8T925	SEQUENCE FROM N.A.		
AC			

RT Whole genome sequencing of meticillin-resistant *Staphylococcus*
 RT *aureus*;
 RL Lancec 357:1225-1240(2001).;

DR EMBL; AP003359; BAB56513.1; -.

DR InterPro; IPR003130; BAB41563.1; -.

DR InterPro; IPR003593; AAA ATPase.

DR Pfam; PF00005; ABC tran.; 1.

DR ProDom; PDD00006; ABC transporter; 1.

DR SM00382; AAA.1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 280 AA; 31464 MW; 2B0B9CF7F341652 CRC64;

Query Match 61.5%; Score 40; DB 16; Length 280;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGV 12
 Db 176 DFVAQGGGI 184

RESULT 7

Q8WU15 PRELIMINARY; PRT; 630 AA.

AC Q8WU15; DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Eukaryotic translation initiation factor 4B.

GN EIF4B.

OS *Lapemis hardwickii* (Hardwick's sea snake).

OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Hydrophiinae; Lapeinis.

NCBI_TaxID=8781;

RP SEQUENCE FROM N.A.

[1] Xu A., Wei J., Yang W., Zhao G., Zhong X.; Factor 4B cDNA clone from sea snake;"

RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF165525; AAL54908.1; -.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF000076; rrm; 1.

SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS000030; RRM RNP_1; UNKNOWN.1.

SQ SEQUENCE 630 AA; 71186 MW; E3457B6ED3502A16 CRC64;

Query Match 61.5%; Score 40; DB 13; Length 630;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SDPLAEGGG 11
 Db 18 SDPLAEDGG 26

RESULT 8

Q9U4G5 PRELIMINARY; PRT; 852 AA.

AC Q9U4G5; Q9VQB2; DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DR BCDNA; GH09817 protein.

GN BCDNA; GH09817 OR CG4272.

OS *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Drosophila.

OC Hydroleidae; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

[1] RN [1] SEQUENCE FROM N.A.
 RP [1] STRAIN=BERKELEY;
 RC [1] RX [1] MEDLINE=20196006; PubMed=10731132;
 RA [1] Adams M.D., Celtnikar S.B., Holt R.A., Evans C.A., Gocayne J.D.,
 RA [1] Amatiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA [1] George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA [1] Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA [1] Brandon R.C., Rogers Y.H.C., Blazej R.G., Champé M., Pfeiffer B.D.,
 RA [1] Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
 RA [1] Abril J.F., Agbyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA [1] Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA [1] Beeson K.Y., Benos P.V., Berman B.P., Bhandaari D., Bolshakov S.,
 RA [1] Boricova D., Botchan M.R., Bouch J., Brokstein P., Brottier P.,
 RA [1] Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA [1] Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,
 RA [1] Dabholkar A., Delcher A., Deng Z., Dietz S.M., Mays A.D., Dew I.,
 RA [1] Dodson K., Doop L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA [1] Durkin K.J., Evans C., Ferraz C., Fleischmann W.,
 RA [1] Foster C., Gabrialian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA [1] Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA [1] Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA [1] Hoskin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA [1] Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA [1] Kimmel B.E., Rodira C.D., Kraft S., Kravitz S., Kulp D., Lai Z.,
 RA [1] Laslo P., Lezi Y., Levitt A.A., Li J., Li Z., Lin X.,
 RA [1] Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA [1] Merkulov G., Milashina N.V., Mobarry C., Morris J., Moskrefi A.,
 RA [1] Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,
 RA [1] Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA [1] Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA [1] Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA [1] Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA [1] Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA [1] Svistek S.R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA [1] Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA [1] Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA [1] Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.O.,
 RA [1] Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA [1] Rhee S.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL science 287:2185-2195 (2000).

RN [2] RP SEQUENCE FROM N.A.
 RC [2] STRAIN=BERKELEY;

RA [2] SMART; SM00360; RRM; 1.

DR [2] PROSITE; PS50102; RRM; 1.

DR [2] PROSITE; PS000030; RRM RNP_1; UNKNOWN.1.

SQ [2] SEQUENCE 630 AA; 71186 MW; E3457B6ED3502A16 CRC64;

Query Match 61.5%; Score 40; DB 13; Length 630;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SDPLAEGGG 11
 Db 18 SDPLAEDGG 26

RESULT 9

Q9U4G5 PRELIMINARY; PRT; 852 AA.

AC Q9U4G5; Q9VQB2; DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DR BCDNA; GH09817 protein.

GN BCDNA; GH09817 OR CG4272.

OS *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Drosophila.

OC Hydroleidae; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

Query Match 61.5%; Score 40; DB 5; Length 852;
 Best Local Similarity 63.6%; Pred. No. 1.e+02;
 Matches 7; Conservative 2; Indels 0; Gaps 0;

Qy 1 SEEDFLAEGGG 11
 DR EMBL; AB003583; AAF51264.1; ALT_INIT.

DR FlyBase; FBgn0028085; BCDNA; GH09817.

SQ SEQUENCE 852 AA; 91073 NW; B873C3607203DA4EC CRC64;

Query Match 61.5%; Score 40; DB 5; Length 852;
 Best Local Similarity 63.6%; Pred. No. 1.e+02;
 Matches 7; Conservative 2; Indels 0; Gaps 0;

Qy 1 SEEDFLAEGGG 11
 DR EMBL; AB0181610; ADD55446.1; -.

DR FlyBase; FBgn0028085; BCDNA; GH09817.

RESULT 9

Q9U4G5 PRELIMINARY; PRT; 852 AA.

AC Q9U4G5; Q9VQB2; DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DR BCDNA; GH09817 protein.

GN BCDNA; GH09817 OR CG4272.

OS *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Drosophila.

OC Hydroleidae; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

DT 01-OCT-2001 (TREMBLref: 18, Last sequence update)
 DT 01-MAR-2002 (TREMBLref: 20, Last annotation update)
 DE Hypothetical protein ms13000.
 GN MSL3900.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Phyllobacteriaceae; Mesorhizobium.
 OC NCBI_TAXID=381;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF03059;
 RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Idezawa K., Ishikawa T., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsunaga M., Matsuno A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimpou S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.;
 RT "Complete Genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti".
 RT EMBL; AP003003; BAB50694.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 89 AA; 10058 MW; 5197B7CB06AFCA351 CRC64;

Query Match 60.0%; Score 39; DB 16; Length 89;
 Best Local Similarity 61.5%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 SESDFLAEGGGV 13
 25 SEVEFVATDGSGL 37

RESULT 10

Q9P8L5 PRELIMINARY; PRT; 171 AA.
 ID Q9P8L5;
 AC Q9P8L5;
 DT 01-OCT-2000 (TREMBLref: 15, Created)
 DT 01-OCT-2000 (TREMBLref: 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLref: 21, Last annotation update)
 DE ABC transporter-like protein (Fragment).
 GN BCATR.
 OS Botryotinia cinerea (Botryotinia fuckeliana).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
 OC Helotiales; Sclerotiniaceae; Botryotinia.
 OC NCBI_TAXID=40559;_
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=B05.10;

RA Schoonbeek H., Vermaulen T., Hayashi K., De Waard M.A.;
 RT "Differential expression of membrane-bound transporters in Botryotinia
 cinerea";
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF238228; AAF61438.1; -.
 DR InterPro; IPR004147; ABC1.
 DR Pfam; PF03109; ABC1; 1.
 PT NON_TER 1 1
 PT NON_TER 171 171
 SQ SEQUENCE 171 AA; 19561 MW; 15515C19C9FB1F9 CRC64;

Query Match 60.0%; Score 39; DB 3; Length 171;
 Best Local Similarity 70.0%; Pred. No. 41;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 SDFLAEGGGV 12
 159 SDFMENGGGV 168

RESULT 11

Q9F7D5 PRELIMINARY; PRT; 186 AA.
 ID Q9F7D5;
 AC Q9F7D5;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=L712;
 RX MEDLINE=21172062; PubMed=11274105;
 RA Price-Carter M., Tingey J., Bobik T.A., Roth J.R.;
 RT "The Alternative Electron Acceptor Tetraphthioboronate Supports Bi2-
 RT Dependent Anaerobic Growth of *Salmonella enterica* Serovar Typhimurium
 RT on Ethanolamine or 1,2-d-propanediol.;"
 RL J. Bacteriol. 183:2463-2475 (2001).
 DR EMBL; AF282268; AAG31761.1; -.
 KW Hypothetical protein.
 FT NON_TER 186 AA; 20711 MW; 6B5FED0B04E07CFA0 CRC64;

SQ SEQUENCE 186 AA; 20711 MW; 6B5FED0B04E07CFA0 CRC64;
 Query Match 60.0%; Score 39; DB 2; Length 186;
 Best Local Similarity 60.0%; Pred. No. 45;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SDFLAEGGGV 12
 102 ADYVAEGGGGL 111

RESULT 12

Q8Z6K4 PRELIMINARY; PRT; 245 AA.
 ID Q8Z6K4;
 AC Q8Z6K4;
 DT 01-MAR-2002 (TREMBLref: 20, Created)
 DT 01-MAR-2002 (TREMBLref: 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLref: 21, Last annotation update)
 DE Orf 245 protein.
 GN STR1741.
 OS *Salmonella typhi*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Salmonella*.
 OC NCBI_TAXID=601;_
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=CP18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Partill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moulle S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 enterica serovar Typhi CT18.";
 RT Nature 413:848-852 (2001).
 RL EMBL; AL627271; CAD01984.1; -.
 DR InterPro; IPR003006; IG_MHC.
 DR PROSITE; PS00590; IG_MHC; UNKNOWN 1.
 KW Complete proteome.
 SQ SEQUENCE 245 AA; 27429 MW; 11BF3BA03D62E3E3 CRC64;

Query Match 60.0%; Score 39; DB 16; Length 245;
 Best Local Similarity 60.0%; Pred. No. 61;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SDFLAEGGGV 12
 102 ADYVAEGGGGL 111

Search completed: February 10, 2003, 16:02:46
Job time : 95 secs